

	Query Match	Score	98.4%; DB 6;	Length	1017;
	Best Local Similarity	98.6%; Pred. No.	3e-108;		
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Db	1	AAGGAAGGTGGAGAAACACAGCAGAACTGGCCAACTGTGATCTTGCCACCGGCGGCACC	60		
Oy	61	ATCGCCGGCGGTGGCGCGCAGCGCGGCGCAACAGCGCCACTTACCAAGGCTGCCAAGGTTGGC	120		
Db	61	ATCGCCGGCGGTGGCGCGCAGCGCGGCGCAACAGCGCCACTTACCAAGGCTGCCAAGGTTGGC	120		
Oy	121	GTGCACAAAGCTGATTTGGCCGGCGCTGCCAGCTGSCCAACTGTGCGCGGCGAG	180		
Db	121	GTGCACAAAGCTGATTTGGCCGGCGCTGCCAGCTGSCCAACTGTGCGCGGCGAG	180		
Oy	181	CAGGTGATGCGATTCGCGCTCCGAAAGATCAACCAACGACGACCTGTCAAGCTGGCAAGC	240		
Db	181	CAGGTGATGCGATTCGCGCTCCGAAAGATCAACCAACGACGACCTGTCAAGCTGGCAAGC	240		
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sequence similarity; putative"
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gene
CDS

gene
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Matches 902; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

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DB 85051 AAGGAGTGGAGAACGACAGACAGACTGGCCAACTGTGTGATCTGGCCACCGCGGCAAC 60

QY 61 ATCCCGCGCGTGGCG 120
DB 84991 ATCCCGCGCGTGGCG 120

QY 121 GTGCAAGAGTGAATGGCG 180
DB 84991 GTGCAAGAGTGAATGGCG 180

QY 181 CAGGTGATGCAGATCGCTCCGAAAGATCAACAGACGACTGTCTCAAGCTGGCAAGC 240
DB 84871 CAGGTGATGCAGATCGCTCCGAAAGATCAACAGACGACTGTCTCAAGCTGGCAAGC 240

QY 241 AGCGTGGCGAGCTGGCG 300
DB 84811 AGCGTGGCGAGCTGGCG 300

QY 301 GACACCGTGAAGAAACCGCTACTTTTGAACCTCGTGAAGAAACCGACCGACCGATC 360
DB 84751 GACACCGTGAAGAAACCGCTACTTTTGAACCTCGTGAAGAAACCGACCGACCGATC 360

QY 361 GTCTGTGTCGTTTCATGCG 420
DB 84691 GTCTGTGTCGTTTCATGCG 420

QY 421 TACAACCGCGTGGCG 480
DB 84631 TACAACCGCGTGGCG 480

QY 481 ATGAACGACGAGATCGATCG 540
DB 481 ATGAACGACGAGATCGATCG 540

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Oy		781	TGCGGGGTGTGTGCGAGCCTTGCAGAGCTGCGCANAAAGCGGTGCAGATCATTTGTTG	840
Db		3737	GCGGCGGTGTGCGAGCCTTGCAGAGCTGCGCANAAAGCGGTGCAGATCATTCGTC	3678
Oy		841	TTAC---GTCAAAGGCGCGTTTGTGTGTGTGAACCGCGAGCGAGCCCGAACAAGAAC	897
Db		3677	TGCAACGTGTAATGCGGCGGCTTGTGTGTGTGTGAACCGCGAGCGAGCCCGAACAAGA	3618
Oy		898	GACTGGGTGTGTGCGCGCAAGCCTTGAACCCGCAAGAAGCGCGCATCTGTGGCATGTGCA	957
Db		3617	GACTGGATGTGTGCGCGCAAGCCTTGAACCCGCAAGAAGCGCGCATCTGTGGCGGTGCG	3558
Oy		958	ATGACCAAGACCAGACAGCAGAGAGCTGCAGCGCATTTTCTGGGAATTACTGA	1011
Db		3557	ATGACCAAGACCAGACAGCAGAGAGCTGCAGCGCATTTTCTGGGAATTACTGA	3504
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Best Local Similarity 83.7%; Pred. No. 4,1e-79;
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Db ATGCGCGGGCCCGCGCGCAAGCGCGCCCAAGAGGCCACTACCAAGGCTGCGCAAGTTGGC 195
Dy 136 ATGCGCGGGCCCGCGCGCAAGCGCGCCCAAGAGGCCACTACCAAGGCTGCGCAAGTTGGC 195
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Db CAGGTGTTCCAGATTCGCTCGAAAGCTTCAACCAAGCAACCTGTGGAACTGGCGAG 315
Dy 241 AGGTGGCCGAGCTGGCGCGCAAGCAATGAGTGGATGGCATCCCATGGGACC 300
Db AGGTGTTCCAGATTCGCTCGAAAGCTTCAACCAAGCAACCTGTGGAACTGGCGAG 315
Dy 316 ACGTGTCCCAAGCTGGCCGATGAGCAAGAGTGAAGCGCATGTGATACCCAGATAC 375
Db ACGTGTCCCAAGCTGGCCGATGAGCAAGAGTGAAGCGCATGTGATACCCAGATAC 375
Dy 301 GACACCTGTGAAGAAACCGGCTACTTTTGAACCTCGTGAAGAAAGACCGACCAAGCTC 360
Db GACACCTGTGAAGAAACCGGCTACTTTTGAACCTCGTGAAGAAAGACCGACCAAGCTC 360
Dy 376 GACACCTGTGAAGAAACCGGCTACTTTTGAACCTCGTGAAGAAAGACCGACCAAGCTC 435
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Db GTGTGTGATCGATTCATGCGCCCGGCAACCGCATGTCCCGCAAGGATGCTCAACTG 420
Dy 436 GTGTGTGATCGATTCATGCGCCCGGCAACCGCATGTCCCGCAAGGATGCTCAACTG 495
Db GTGTGTGATCGATTCATGCGCCCGGCAACCGCATGTCCCGCAAGGATGCTCAACTG 495
Dy 421 TACAAACCCGTGGCGCGTGGCAAGCAAAAGCTGGCGGCAAGGGCGTGGTGAAC 480
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Dy 496 TACAAACCCGTGGCGCGTGGCAAGCAAAAGCTGGCGGCAAGGGCGTGGTGAAC 555
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Dy 481 ATGAACACAGAGATTCAGTCCGGGCTGTGACGTGAGCAATGTCATCAATCAAGACGAA 540
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Dy 556 ATGAACACAGAGATTCAGTCCGGGCTGTGACGTGAGCAATGTCATCAATCAAGACGAA 615
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Dy 541 GCTTTCAAGAGCGCTGGGGCCCGCTGGGCAATGTTGTAAGGCAATGTCATGTTTC 600
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Dy 721 CTGGCAACAAGACCGCGCCAAAGCGCTGATTCATGCGCGCAACCGGCAATGGCTCGTGTG 780
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Dy 796 CTGGCCCAAGGCGGCGCCAAAGGAGATTCATCATGCGCGCAACCGGCAATGGCTCGTGTG 855
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Dy 841 TCAC---GTACACAGGGCGGTTTCGTGCTGGTGAACCGCGAGCGCCGACGACCAAGAC 897
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Df		976 GACTGATGATGTGCCCAACGACTGAACCCGAGAAAGGCGCGATCTGTGGCGGGTCSG 1035
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LOCUS		
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ACCESSION	Pseudomonas fluorescens glutaminase-asparaginase precursor, gene,	
VERSION	complete cds.	
KEYWORDS	AP056495	
SOURCE	AF056495.1 GI:3044186	
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REFERENCE	Pseudomonas fluorescens	
AUTHORS	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	
TITLE	Pseudomonadaceae; Pseudomonas.	
JOURNAL	1 (bases 1 to 1709)	
MEDLINE	Huser,A., Klopner,U. and Rohm,K.H.	
PUBMED	Cloning, sequence analysis, and expression of ansB from Pseudomonas	
REFERENCE	fluorescens, encoding periplasmic glutaminase/asparaginase	
AUTHORS	FEMS Microbiol. Lett. 178 (2), 327-335 (1999)	
TITLE	99429098	
JOURNAL	10499283	
MEDLINE	2 (bases 1 to 1709)	
PUBMED	Koehn,K.H. and Huser,A.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (01-Apr-1998) Physiol. Chemie, Uni-Marburg, Karl von	
TITLE	Fritsch Str.1, Marburg/Lahn D - 35033, Germany	
JOURNAL	Location/Qualifiers	
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ORIGIN		
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Oy		61 ATTCCCGGCGGCTGGCGCCAGCGCGCGCCAAACGCGCACTTACGAGCTGCGCAAGATTGC 120
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REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1	Hueser, A., Kloeppner, U. and Roehm, K. H.	Cloning, sequence analysis, and expression of anab from <i>Pseudomonas fluorescens</i> , encoding periplasmic glutaminase/asparaginase	FEBS Microbiol. Lett.	178, 327-335 (1999)	2	(bases 1 to 2353)	Roehm, K. H.
		Direct Submission					
		Submitted (03-MAY-1999)	Roehm K. H., Inst. f. physiol. Chemie, Uni-Marburg, Karl-von-Frisch-Str. 1, D-35033 Marburg/Lahn, GERMANY				
		Location/Qualifiers					
		1. .2353					

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CR543861_35 3500001 3598621
Continuation 721 of 36) of CR543861 from base 2000001 (CR543861 *Actinobacter* sp. ADPI c

Query Match	30.9%	Score 313	DB 1	Length 110000
Best Local Similarity	58.7%	Pred. No. 6.9e-29		
Matches 582	Conservative	0	Mismatches 400	Indels 9
			Gaps	2

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 Db 71179 AACGTCGTGTAGTCGCAACAGTGTGAACAAATGCGCGGTCCGGGCGCAAGCTCCACCAAC 71238
 QY 91 AGCGCACTTACACAGGCTGCCAAGGTTGCGCTGCACAAGCTGAATTTGCGCGGTGCCGAG 150
 Db 71239 AGTGCACACTTATCTGCGAGCAAAAGTACCAATCGATGCACTGATCAATGCAAGTACTCA 71298
 QY 151 CTGGCCGACCTGGCCCATATGCGCGCGGCGAGCAAGTATGCAATGCGCTCCGAAAGCATC 210
 Db 71299 ATCAAAGATTTGGGCGCAATGTAAAGCGGCATTCMAAGCTTTACAAATCGCGTCTGAAGATAT 71358
 QY 211 ACCAAGCGACGACTGCTCAAGCTGGCAAGCGCGGCGGCGGCGGCGGCGGACAGCAATGAC 270
 Db 71359 ACTGCACAAAGATTTATTTCTCTTGGCCGCGCAAGTTAATGATCTTGTAAAAAACATCT 71418
 QY 271 GTCATGCGCATCGTCATCAACCCATGCGCACCGACACCTTGAAGAAACCGCTTACTTTTGG 330
 Db 71419 GTAAATGGTGTGTGATTACACATGGTACATGATACGCTTGAAAGAAACAGCTTTCTTTTAA 71478
 QY 331 AACCTCGTGAAGAAAGCCGACAAAGCCGATCGTCTGTGCTCGTTCCATGCGCCCGGCAAC 390
 Db 71479 AATCTTGTGATTCTACGGAATMAACCAATGTTCTGTGTGTCTTAATGCGGCCCATCAACA 71538
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 Db 71599 GAAACAAATAAATAAAGCGGTATGTATGATGATTCATCTTTGACGACGATGAT 71658
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 Db 71959 AATATTACATGATGAAACAAGGGATTCATATCATTCGCGCTCATCAGGTGATACGCAAGGTTTC 72018
 QY 862 GTGCTGTGCTTAACGCGGAGCAGCCGACGACGACAAAGCACTGGGTGTGCGGCCACGACCTG 921
 Db 72019 GTATTTGGTAAATGCGCAACACCTGATGATCAATATGCTGGGCGGTGTGCAATGATTTA 72078
 QY 922 AACCCGAGAAAGCGCCGATCTGTGCGATGTGTGCAATGACCAAGCCACAGACAGCAAG 981
 Db 72079 AATCAACAAAAGCAAGCTGTGCTTGTGCTTGTAGCATGCAAAAACCAATGATGACAAA 72138
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Db 72139 GAAATCCAGCGTATGTTCTGGCAATATTAAT 72169

RESULT 8
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WPCOMMENT

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BX571965_03	300001	410000
BX571965_04	400001	510000
BX571965_05	500001	610000
BX571965_06	600001	710000
BX571965_07	700001	810000
BX571965_08	800001	910000
BX571965_09	900001	1010000
BX571965_10	1000001	1110000
BX571965_11	1100001	1210000
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BX571965_29	2900001	3010000
BX571965_30	3000001	3110000
BX571965_31	3100001	3210000
BX571965_32	3200001	3310000
BX571965_33	3300001	3410000
BX571965_34	3400001	3510000
BX571965_35	3500001	3610000
BX571965_36	3600001	3710000
BX571965_37	3700001	3810000
BX571965_38	3800001	3910000
BX571965_39	3900001	4010000
BX571965_40	4000001	4074542

Continuation (17 of 41) of BX571965 from base 1600001 (BX571965 Burkholderia pseudomalle)

Query Match	27.9%;	Score 283.2;	DB 1;	Length 110000;	
Best Local Similarity	57.9%;	Pred. No. 2.5e-25;			
Matches 545;	Conservative	0;	Mismatches 388;	Indels 9;	Gaps 2;
24	GCTGGCAACGCGATCTCTGGCCACCGGCGCACATCGCGGCGCTGGCGCACGCGC	83			
83770	GCTGGCGGCGCATCGCGCTCTCGCAGCGGCGCGCACATCGCGGCGCGCGCCGACGCGC	83829			
84	GCGCCACAGCGCCACACTACCAAGCTGCGCAAGTTGGCGTGCACAGCTGATTGCGGCGGT	143			
83830	CGCGCAGACGCGCGCGCTACCAAGCGGCGCGCGCTCGCGTGCACAGCTGCTCGCGCGGT	83889			
144	GCGGAGCTGGCGCGCATCTGGCCCAATGTGCGCGCGCGCAGGTGATGCAATCGCTTCGGA	203			
83890	GCGCGCGCTCGCGCGCATGCGCACATCGAGGCGCGCAGGTGCGCAGCATTCGACACCAA	83949			
204	AAGCATCACCAACGACGACCTGCTCAAGCTGCGACAGCGTGGCGAGCTGGCGCGACAG	263			
83950	GGACTTGTGCGCGCGCGCTGTGACGACGCTTCGCGAGCGGATGACCGCGCTTGGCGGAA	84009			
264	CAATGACGTGATGCGATCGTATCATCCCATGCGACCGACACCTCTGAGAGAAACCGCTTA	323			

[illegible]

RESULT 10

LOCUS	A27539	300 bp	DNA	linear	PAT 20-SEP-1995
DEFINITION	Pseudomonas 7A glutaminase gene N-terminal.				
ACCESSION	A27539				
VERSION	A27539.1	GI:1247712			
KEYWORDS	.				
SOURCE	Pseudomonas sp.				
ORGANISM	Pseudomonas sp.				
REFERENCE	Bacteria; Proteobacteria.				
AUTHORS	1 (bases 1 to 300)				
JOURNAL	.				
FEATUERS	Patent: DE 4140003-A 1 09-JUN-1993;				
	Location/Qualifiers				
source	1..300				

CDS

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/db_xref="GI:1247713"
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ORIGIN

Query Match	Similarity	27.7%	Score 281	DB 6	Length 300
Best Local	Similarity	96.0%	Pred. No. 2e-24		
Matches	287	Conservative	0	Mis-matches	12
				Indels	0
				Gaps	0
QY	1	AAGGAAGTGAAGAAC	CAGCAGAGAGTGGC	CAACGTCGTGATCTCTGGCCACCGGCGGCAC	60
DB	1	AAGGAAGTGAAGAAC	CAGCAGAGAGTGGC	CAACGTCGTGATCTCTGGCCACCGGCGGCAC	60
QY	61	ATCCGCGCGCTGGCGCCAGCGCGCC	CAACAGCGCCACTTAC	CAAGCTTCCAGGTTGGC	120
DB	61	ATCCGCGCGCTGGCGCCAGCGCGCC	CAACAGCGCCACTTAC	CAAGCTTCCAGGTTGGC	120
QY	121	GTCCAGCAAGCTGATTGGCCGGCGCTG	CCGAGCTGGCCGA	CTTGGCCMAATGTGCGCGCGAG	180
DB	121	GTCCAGCAAGCTGATTGGCCGGCGCTG	CCGAGCTGGCCGA	CTTGGCCMAATGTGCGCGCGAG	180
QY	181	CAGGTGATGCAAGATGCTCCGAAAGCAT	CACCAACGACGACTGCTCA	AGCTGGCAAGC	240
DB	181	CAGGTGATGCAAGATGCTCCGAAAGCAT	CACCAACGACGACTGCTCA	AGCTGGCAAGC	240
QY	241	AGCGTGGCGGAGCTGGCCGACAGCA	ATGACGTGCATGCTCATCA	CCCAATGGCAC	299
DB	241	AGCGTGGCGGAGCTGGCCGACAGCA	ATGACGTGCATGCTCATCA	CCCAATGGCAC	299

RESULT 11

LOCUS	AR319786	1125 bp	DNA	PAT 17-AUG-2003
DEFINITION	Sequence	2336	from patent US 6562958.	
ACCESSION	AR319786			
				linear

VERSION AR319786.1 GI:33700889
 KEYWORDS
 SOURCE
 ORGANISM Unknown.
 Unkown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1125)
 AUTHORS Breton,G. and Bush,D.
 TITLE Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics
 JOURNAL Patent: US 6562958-A 2336 13-MAY-2003;
 FEATURES Location/Qualifiers
 SOURCE 1..1125

ORIGIN

Query Match	Similarity	Score	DB	Length
Beet	Local	56.2%	Pred. No. 1.3e-231	
Matches	557	Conservative	0	Mismatches 425; Indels 9; Gaps 2
QY	30	CAAGCTGTGATNCTTGCGCCAGCCGGCGGACCATCGCCCGCTGGCGCCAGCGCGGCCAA	89	
DB	135	CAATGTTGTGTGTGTGTCGTACTGGCGGTGACCATTTGCTGTGTCTGGCGCAAGCTCAGCAA	194	
QY	90	CAGGCGCACTTACCAAGGCTGCGCAAGGTTGGCGTGCACAAGCTGATTTGCCGGCGTGC	149	
DB	195	TAGTGCACATTTATACGGCGGCAAAAGTTCCAGTTGATGCTTTAATCAATGACAGTTCTCA	254	
QY	150	GCTGGCGCACTTGGCGCAATGTGTGGCGGAGACAGGTGATGAGATTCGCTCCGAAAGCAT	209	
DB	255	AATTCAGATTTGGCGGATGTATCTGTGTATCCAGCATTTACAGTAGCTTTCTGAAGATAT	314	
QY	210	CACCAACGACGACCTGCTCAAGCTGTGGCAAGCGGTGGCCGAGCTGGCGCGACAGCATGA	269	
DB	315	TACTGACAGAGAAATTTATTAACAATTTGCTGCTCAAGTAAATGAATCTGTTAAAGGCAAC	374	
QY	270	CGTGCATGCGATTCGTCAATCAACCATGAGACCGACACCTGTGAAGAAACCGCTACTTTT	329	
DB	375	TGTAAATGCGCTGTGATTTACACCGGTACAGATTCCTTTAAGAAAGACGATTTTCTT	434	
QY	330	GAACCTCGTGGAAAAAGACCGACCAAGCCGATGCTGTGTGCGTTTCATGCGCCCGCGAC	389	
DB	435	AAATCTGTGTGTCACTGATTAACCAATGTGTAATTTGTGGCTCAATGGCCCATTAAC	494	
QY	390	CGGCATGTCCGCGCGACGCGATGCTCAACTGTATCAAGCGCGTGGCGGTGGCCAGCAACA	449	
DB	495	TGCTCTTTCAACAAGATGTGTCACTTAACCTTTATAGTGCTGTGTGATTTGGCGCTTCTGA	554	
QY	450	GAGCTCGCGCGGCAAGGGCGTGTGCTGTGACATGAACGACGATTCAGTCCGGGCGTGA	509	
DB	555	TGATGCAAAAAATTAAGCGGTTATGTGTTCTATGAACGATCTATTTTGTGCTGCGTGA	614	
QY	510	CGTGAAGCAAGTCATCAATCAAGACCGAGCTTCAAGACGCGCTTGGGCGCGCTGGG	569	
DB	615	TGTAACTTAAGGCAATTAACATTCATCAACAAATGCTTTGTGAAGCAATGGGTGCTTTGG	674	
QY	570	CATGTGTGTGAAGGCAAGTGTGTACTGTGTTCCGCTGTGCGGCGCAAGCGCCACAGGTCAA	629	
DB	675	TACACTGTGTGAAGGCAAAACCATTTGTGTTAAGCAATCTGTTTAAACGTCAATCAATGC	734	
QY	630	CTCCGAGTTCACATCAAGCAGATCAGCAGC-----CTGCGCCAGGTGACATTCGCTTA	683	
DB	735	TTTCAGATTTAATTTGAAATATTTAAGGTGATGTCTTCCGACAGTACAAATGCTTTA	794	
QY	684	CAGCTATGCAAGTCAACCGACCGGCGCTTCAAGGCGCTTGGCAACAAGCGCGCCAGAGGC	743	
DB	795	TGTGTTCTGACCTTATGTCTTCTCTGATGCTTTAAGAGCATATGCAAAAGCTGCGCTTAAGC	854	
QY	744	GCTGATCAGTCCGCGCACCGGCATATGGCTGTGTGTGCGCGGGGTGGTCCAGGCGCTGCA	803	
DB	855	GATTAATTCATGACAGGTACAGGTAAATGTGTTCTGTAGCGAAATATATCGTTCCAACTTACA	914	
QY	804	GAGACTGC--GCAAGAACGGCGTGCAGATCATTTGTTGTCAGCTCAACAGGCGGTTT	860	

Db 915 AACCTTCATGACAAAACGGTATTCCTCAATATTCCTGCTCATCGCGCTTCCACAAGGTTT 974
 Qy 861 CGGCTGCGTAAAGCCGAGGAGCCGACGACAAAGACGAGCTCGTGCGCCAGCAGCT 920
 Db 975 TGTATTACGATATCAGAAACCACTGACTTAAATATGTTGGTGTAGACAGCTCATGATTTT 1034
 Qy 921 GAACCCGACAGAGCCGCGCATCTCGCGATGCTGCGCAATGACCAAGCCAGACAGCA 980
 Db 1035 GAATCCCTCAAAAAGCGGTCTTCTTGCGGCGTTGGCATTACCAAAAACAACGATGGAA 1094
 Qy 981 GAAGCTGACGCGCATTTTCTGGGAATCTGA 1011
 Db 1095 AGAATTCACACGCAATGTTCTGCGAGTACTTA 1125

RESULT 12
 ECASN 1399 bp DNA linear BCT 31-MAR-1995
 LOCUS Erwinia chrysanthemi asn gene for L-asparagine aminohydrolyase (EC 3.5.1.1).
 ACCESSION X12746.1 GI:40993
 VERSION X12746
 KEYWORDS asn gene; hydrolase; L-asparagine aminohydrolyase.
 SOURCE Erwinia chrysanthemi (Pectobacterium chrysanthemi)
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pectobacterium.
 REFERENCE 1 (bases 1 to 1399) Palford, S. and Anderson, D.M.
 AUTHORS Filipula, D., Nagle, J.W., Palford, S. and Anderson, D.M.
 TITLE Sequence of L-asparaginase gene from Erwinia chrysanthemi NCPPB 1125
 JOURNAL Nucleic Acids Res. 16 (21), 10385 (1988)
 MEDLINE 89057497
 PUBMED 3194219
 REFERENCE 2 (bases 1 to 1399)
 AUTHORS Filipula, D.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-1988) Filipula D., Genex Corporation, 16020 Industrial Drive, Gaithersburg, MD 20877, USA

FEATURES
 source location/Qualifiers
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 123..129
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 223..1269
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 RIKDLTTRSGVDFRG.LSLPKVDILYGYDDPEYLDAALQHGKVIIVVAGMGASV
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ORIGIN
 Query Match 26.3%; Score 266.4; DB 1; Length 1399;
 Best Local Similarity 55.9%; Pred. No. 7.5e-23;
 Matches 557; Conservative 0; Mismatches 421; Indels 18; Gaps 2;

Qy 20 AGAAGCTGSCCAAGTGTGATCTTGGCCACCGGCGGACCAATCGCGGCGTGGGCCA 79
 Db 290 ATTAACCTGCCAATATCGTTATCTTGGCCACCGGCGGATCTATATGCGGTCGCGCA 349
 Qy 80 GCGGCGCAACAGCGGCACCTATCAGAGTGGCCAGGTTGGCGTGCACAAGCTGATTGCG 139
 Db 350 CGGGTACCCCAACACAGGGTTACAGAGCTGGCGCGCTTGGCGTGGATAGCTTAATCAAG 409
 Qy 140 GCGTGGAGTGTGGCCGACCTGGCCCAATGTGGCGCGGAGAGGATGATGAGATCGCT 199
 Db 410 CTGTGCTGAGTGAAGAACTGGCTAATGTGAAGGGGAGGAGCTTCTCAACATGGCCA 469
 Qy 200 CCGAAGACATCACCAACAGACAGCTCTCAAGTGGGACAGCGTGGCGGACTGGCCG 259
 Db 470 GCGAATAACATGACCGGTGATGTGGTCTCAAGCTGAGCCAGCGGTGAATGAATCTGTGG 529
 Qy 260 ACAGCAATGACGTGATGGATGTCATCATCAACCATGAGCCGACCCCTGGAAGAAACG 319
 Db 530 CACGGATGATGTGATGTGTGTGATCAACCGGTACCGACACTGTGGAAGATCGG 589
 Qy 320 CTTACTTTTGAACCTCTGGAAAAGACCGACAGCCGATCGTGTGTTCCATGC 379
 Db 590 CTTACTTTTCTTCACTGACGGTAAAGATGAACAGCCGGTGTGTGTGCGACGATGC 649
 Qy 380 GCCCGGACCGCCATGTCCGCGACGCGCATCTCAACTGTACCAAGCCGTGGCGGTGG 439
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 Qy 440 CCAAGCAACAGAGCTGCGCGCGGCAAGGCGTGTGATGACATGAACGAGATCCAGT 499
 Db 710 CGGGTGTAGACGTCTCGCGGCTGTGGCTGTGATGTGTGATGATGATCGATCGGCT 769
 Qy 500 CCGGGCGGTGACGTGACCAAGTTCATCAACCAAGCCGAGCTTC--AAGAGCGCT 556
 Db 770 CTGCGCGCTCATCAACCAAGACCAAGCCCTCTACGCTGATGATGATCGATCGGCT 829
 Qy 557 GGGGCGCGTGGCATGTGTGTGGAAGGCAAGTCTGATCGTTCGCGTCCGCGCAAGC 616
 Db 830 AAGGCTACCTGGGCGTTATCATGTGATGGAACCGCATTTACCAAAACCGTATGACAAAGC 889
 Qy 617 GCCACACGGTCACTCCAGTTTCAGATCAATCAAGACGATCAGACGCTGCCAGGTGACA 676
 Db 890 TGCATACCAACCGGTGTGTGTGATGAGGTGTGATGATGATGATGATGATGATGATGATG 949
 Qy 677 TCGCTACAGCTATGCAACGTGACCGACCGCTTCAAGGCTTGGCAGAGAGCGG 726
 Db 950 TTTCTTATGCTATCAGATGACCGGAAATATCTGATGACGCGGCTATCACAGATGGCG 1009
 Qy 737 CCAAGCGCTGATTCATGCTGCGGACCGGCAATGGCTCGGTGTGCGGGGTGTGCGAG 726
 Db 1010 TAAAGGTATCGTCTATGCGGATGAGGCGGGGTTCAAGTGTGCTGTGTATGTCGCG 1069
 Qy 797 CCGTGAAGAGTGTGCGCAAGACGCGGTGAGATCATTCGTTGTCGTCACGTCACAGGCG 856
 Db 1070 GCATGCGCAAGGCGCTGGAAGAAAGGCGTTTGTGTATGCTTATCTGCAAGCGCATG 1129
 Qy 857 GTTTCGTGCTGCTGAACCGCGGACAGCCGACGACCAAGAAAGCATGCGGTGTGGCCACG 916
 Db 1130 GTATTGTGCGCGCGATGAAGAGCTGCAAG-----GTCGTGTTTCTGACT 1174
 Qy 917 ACCTGAACCGCGAAGAGCGCCGATCTGCGCATGTGTGATGATGATGATGATGATGATGATG 976
 Db 1175 CTCTTAACCGCGACATGCTGCGATCTGTGTATGCTGCGGATTAATGACCAAGTATC 1234
 Qy 977 GCAAGAGCTGACGCGCATTTCTGGGAATACTGAT 1012
 Db 1235 CGAAGTCATTCAAGAGTATTTTCATCATCTTATGAT 1270

RESULT 13
 AY560098 1047 bp DNA linear BCT 22-MAR-2004
 LOCUS Erwinia chrysanthemi L-asparaginase precursor gene, complete cds.
 DEFINITION

ACCESSION AY560098
 VERSION AY560098.1 GI:45505306
 KEYWORDS
 SOURCE
 ORGANISM
 Brvlinia chrysanthemi (Pectobacterium chrysanthemi)
 Brvlinia chrysanthemi
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Pectobacterium.
 REFERENCE
 AUTHORS
 1 (bases 1 to 1047)
 Kozia, G.A. and Labrou, N.E.
 Cloning, expression and characterization of L-asparaginase from
 Brvlinia chrysanthemi 3937
 JOURNAL
 TITLE
 Unpublished
 2 (bases 1 to 1047)
 Kozia, G.A. and Labrou, N.E.
 Direct Submission
 REFERENCE
 AUTHORS
 Submitted (26-FEB-2004) Agricultural Biotechnology, Agricultural
 University of Athens, 75 Iera Odos, Athens 118 55, Greece
 JOURNAL
 TITLE
 Location/Qualifiers
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 20 AGAAGCTGGCCAGATGATGATCTGGCCACCGGCGGACCATCGCGCGCTGGCGCA 79
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 128 CGGGTACCCAGACTACCGGTTACAAAGCGCGCGCTGGCGTGGATACGCTGATCAACG 187
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 200 CCGAAGCATCATCAACGACGACCTGCTCAAGCTGGCGCAAGCGGCTGGCGCGCGCG 259
 248 GCGAAAACATGACCGCGCATGTGTCTGAAACTGACGACGCGGTGAATCGCTGCTGCG 307
 260 ACAGCAATGACGTGATGATGCTCATCAACCGATGCGACCGACACCTGTGAGAAAAACG 319
 308 CGCGTACGATGTGACGCGCTGTGATTAACCAACGTAACGACACGCTGAGAGATCGG 367
 320 CCTACTTTTGAACCTGCTGTAAGAAAGACCGAATCGTGTGCTGCTTCATGCG 379
 368 CCAATTTCTCTACCTGACGCTGAAAGCGACCAAGCGGTAGTGTGTTCGCGCGCGATGC 427
 380 GCCCGGACCGCGCATGTCGCGCGACGCGCATGCTCAACCTGTACAAAGCGCGTGGCGGTG 439

Db 428 GCCCGGACAGCGCATTAAGCGCGACCGGCCGATGAACCTGTGAAAGCGTTGCGGTG 487
 Qy 440 CCAGCAACAGAGACTCGCGCGCGCAAGCGCTGTGTGTGACCATGAACAGATCCAGT 499
 Db 488 CGAGCGACAAACAGTCTCGCGCGCGCGCGCTGTGTGTGTGCTCAACACGATTCGCTT 547
 Qy 500 CCGGCGCGTGAAGTGAAGAGTGAATCAATCAACAGACCGAAGCGTTCA---GAGCGCT 556
 Db 548 CCGCGCGTTATATACCAAGACCAATGCTGACGCTGGAACAGTTTCGGCGGATGAAG 607
 Qy 557 GGGGCGCGCTGGAGATGTGTGTGAAGGCAAGTGTACTGTGCTCGCTGCGCGCAAGC 616
 Db 608 AAGGTATCTGGGGGTGTGTGTGATCGGTAAACATATCTATACAGAAATGCTTCAGAAC 667
 Qy 617 GCGACAGGTCACTCCGAGTTTCAATCAACAGATGACAGCGCTGCCAGGTGAC 676
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 Qy 737 CCAAGCGCTGATCCATGCGCGCACCGCATGTGCTGTGCTGCGCGGTGTGCGAG 796
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 Qy 917 ACTGAAACCGCGAAGAGCGCGCATCTGCGGATGTGTGCGCATGACCAAGACCGAGCA 976
 Db 953 CGCTCAACCGCGCGCATGCGCGATCTGTGTAAGTGTGCGCATGACCGACCGAGCATC 1012
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 Db 1013 CGCGGTGATTCAGACTATTTCCACACTATTGA 1047
 RESULT 14
 BX640423 348251 bp DNA linear BCT 06-MAY-2004
 LOCUS
 DEFINITION
 1/14.
 BX640423 BX470249
 VERSION
 BX640423.1 GI:33564799
 KEYWORDS
 complete genome.
 SOURCE
 Bordetella parapertussis
 ORGANISM
 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 Alcaligenaceae; Bordetella.
 REFERENCE
 AUTHORS
 1
 Parkhill, J., Sebatia, M., Preston, A., Murphy, L.D., Thomson, N.,
 Harris, D.E., Holden, M.T.G., Churcher, C.R., Bentley, S.D.,
 Mungall, K.L., Cerdeno-Tarraga, A.M., Temple, L., James, K., Harris, B.,
 Quail, M.A., Achtman, M., Atkin, R., Baker, S., Basham, D., Bason, N.,
 Cherevach, I., Chillingworth, T., Collins, M., Cronin, A., Davis, P.,
 Doggett, J., Felwell, T., Goble, A., Hamlin, N., Hauser, H.,
 Holtroyd, S., Jagsels, K., Leather, S., Moulis, S., Norbertzak, H.,
 O'Neill, S., Ormond, D., Price, C., Rabinowitsch, E., Rutter, S.,
 Sanders, M., Saunders, D., Seeger, K., Sharp, S., Simmonds, M.,
 Skelton, J., Squares, R., Squares, S., Stevens, K., Unwin, L.,
 Whitehead, S., Barrall, B.G. and Maskell, D.J.
 Comparative analysis of the genome sequences of Bordetella
 pertussis, Bordetella parapertussis and Bordetella bronchiseptica
 Unpublished
 JOURNAL
 TITLE
 REFERENCE
 AUTHORS
 2 (bases 1 to 348251)
 Direct Submission

Db	5781	GGCCGAGCGCGTGCAGAGGCCGAGACGACTGCGCAGACAGGCTGCGCCGCGGATCGACAT	5840
Qy	678	CGCCTACGACTATGAGCAACGTGACCGACACGCGCTTACAGAGCCCTGSDACAGAACGCGC	737
Db	5841	CGTCACATGCCGTGTGATCGATCTGACCGCGAGCTCATGCAATTTCATGACCGGG---CGAGC	5897
Qy	738	CAAGCGCGTATTCATGCGCGGACCGGCAATGGTCGGTGTGTCGCGGGGTGATGCCAGC	797
Db	5898	CCAGGGCATCTGCTGCGCGCGCGCTGCGGCGACGCGCAACGACCGACCGCGCCCTGCGAGGC	5957
Qy	798	CCTCACGAGAGCTGCGGCGCAAGAACGCGCGTGCAGATCATTCCTTCACATGACGTAACAGGCGCG	857
Db	5958	CCTTCAGCGGGGCTGCGCGCGCGGGCGTTGCGGTGATCGGGCGTCCGCGCACCGGCTCGGG	6017
Qy	858	TTTGTGTGCTGTAAAGCCGAGCAGCCCGACGACAAAGACGACTGGGTCGTGGCCCGACGA	917
Db	6018	CAGGATGGGGGCGCATATTCAGATTCGACGACGAGCGCTGCGGCTTCATTGCGCGCGCGGCA	6077
Qy	918	CCTGAACCCGCGAAGAGGCCGATCCTGAGCGATGCTGAGATGACAGAACCCGACGACAG	977
Db	6078	CCTCAGCCCCAGAAAGGCCGCGCTGCTGCTTACCTTGGGCGCTGTGCCAGAACCGCGATAC	6137
Qy	978	CAAGAGCTGCAG	990
Db	6138	CGCGCGCTGCAG	6150

RESULT 15

LOCUS	BX640437	347356 bp	DNA	linear	BCT 06-MAY-2004
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1/16.

VERSION BX640437.1 GI:33575039

SOURCE	
Bordetella bronchiseptica RB50	

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

REFERENCE

1

Harris, D.B., Holden, M.T.G., Churcher, C.R., Bentley, S.D.,

Quail, M.A., Achtmann, M., Atkin, R., Baker, S., Basham, D., Bason, N.,

Doggett, J., Feltwell, T., Goble, A., Hamlin, N., Hauber, H.,

O'Neil, S., Ormond, D., Price, C., Rabinowitsch, E., Rutter, S.,

Skelton, J., Squares, R., Squares, S., Stevens, K., Unwin, L.,

TITLE Comparative analysis of the genome sequences of *Bordetella*

JOURNAL
Unpublished

AUTHORS
Sebahintia, M.

JOURNAL
Submitted (06-AUG-2003) Submitted on behalf of the Pathogen

Hinxton, Cambridge CB10 1SA, E-mail: m85@banger.ac.uk

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Query Match 26.0%; Score 264; DB 1; Length 347356;
 Best Local Similarity 56.5%; Pred. No. 3.6e-23;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1014	100.0	1014	2	AAQ68438
2	742	73.2	1182	11	ABD07189
3	742	73.2	1135	11	ABD07273
4	562.2	55.4	2748	11	ABD07169
5	281	27.7	300	2	AAQ43365
6	273	26.9	1125	9	ADA31049
7	261.6	25.8	2837	1	AAAT0557
8	252.2	24.9	1044	3	AAK82834
9	240.8	23.7	1848	2	AAT96346
10	240.4	23.7	1071	11	ACH94935
11	219	21.6	1133	2	AAK03474
12	219	21.6	1133	3	AAK62512
13	209.2	20.6	1174	8	ABZ80801
14	207.2	20.4	270	11	ABD07223
15	205.6	19.8	1303	12	AD007178
16	200.6	19.8	1330	12	AD007182
17	189.2	18.7	1128	12	AD136573
18	178	17.6	1137	12	ADN97129
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	23	156.2	15.4	3223	12	ADN97128	ADN97128 ASPA01 as
	24	145.6	14.4	1196	2	AAK14328	AAK14328 H. pylori
	25	138	13.6	110000	2	AAT42063_07	Continuation (8 of
	26	138	13.6	110000	2	AAT42063_08	Continuation (9 of
	27	129	12.7	1041	10	ADP00934	AdP00934 Bacterial
	28	122.8	12.1	1470	12	AD007186	Ad007186 Fusarium
	29	118.2	11.7	1260	12	AD007184	Ad007184 Penicillium
	30	110	10.8	1236	12	AD007188	Ad007188 Penicillium
	31	85.2	8.4	345	6	ABK6196	ABK6196 Helicobac
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	36	78.8	7.8	2772	11	ABD07224	ABD07224 Pseudomon
	37	75.8	7.5	926	12	ACH87387	ACH87387 Human gen
	38	74.6	7.4	1191	8	ACA26934	ACA26934 Prokaryot
	39	72.2	7.1	960	10	ABX07792	ABX07792 S. pneumo
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ALIGNMENTS

RESULT 1	AAQ68438	standard; DNA; 1014 BP.
ID	AAQ68438	
XX	AAQ68438;	
AC	25-MAR-2003 (revised)	
DT	12-JUN-1995 (first entry)	
XX	Pseudomonas glutaminase gene.	
DE		
XX	glutaminase; antiviral; virucide; anticancer; cancer therapy; HIV virus;	
KM	gene therapy; Escherichia coli; ds.	
XX		
OS	Pseudomonas sp.	
XX		
PN	WO9413817-A1.	
XX		
PD	23-JUN-1994.	
XX		
PF	04-DEC-1992; 92WO-US010421.	
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PR	04-DEC-1992; 92WO-US010421.	
XX		
PA	(MEME-) MB MEDICAL ENZYMS AG.	
XX		
PI	Roberts J, MacCallister TW, Sethuraman N, Freeman AG;	
XX		
XX	WPI; 1994-217891/26.	
DR	P-PDB; AAR59739.	
XX		
PT	Recombinant glutaminase derived from Pseudomonas 7A - expressed in E	
PT	coli to increase yield and avoid Pseudomonas endotoxins for antiviral and	
XX	anticancer therapy.	
PS	Disclosure; Page 33; 60pp; English.	
XX		
CC	Chromosomal DNA from Pseudomonas sp. 7A (ATCC 29598) was used to	
CC	construct a genomic library in Escherichia coli LB32. Screening with	
CC	mixed oligonucleotide probes was used to isolate a glutaminase- encoding	
CC	clone. This was sequenced using the primers given in AAQ68439-47. The	
CC	gene can be used to manufacture recombinant glutaminase, free of	
CC	Pseudomonas exotoxin, for use in e.g. HIV and cancer therapy. The gene	

CC may also be used in gene therapy protocols. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 1014 BP; 226 A; 324 C; 318 G; 146 T; 0 U; 0 Other;

Query Match 100.0%; Score 1014; DB 2; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 2,5e-166;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GTGCAACAGCTGATTTCCGCGCTGGCGAGAGCTGGCGCAATGTGGCGGCGAG 180
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QY 361 GTGCGTGTGGTTCATGAGGCGCGGACGCGCATGTGCGCGGAGGAGATGCTGACATG 420
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DB 841 TCACTGCAACAGGCGGCTTCTGTGCTGCTGAACGCGGAGACGCGCAACGAGAGC 900
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QY 961 ACCAAGACCCAGAGACGACGAGAGCTGCAAGGCTATTTCTGGGAATACTGATTA 1014
 DB 961 ACCAAGACCCAGAGACGACGAGAGCTGCAAGGCTATTTCTGGGAATACTGATTA 1014

RESULT 2
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 ID ABD07189 standard; DNA; 1182 BP.
 XX
 XX ABD07189;
 AC
 XX
 DT 29-JUL-2004 (first entry)
 XX

DE Pseudomonas aeruginosa polynucleotide #5793.

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
 KW antibacterial.

OS Pseudomonas aeruginosa.

PN US6551795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, DeLoughery C, Bush D;

DR WPI; 2003-615309/58.

PT P-PsDB; ABO73618.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 useful as molecular targets for diagnostics, prophylaxis and treatment of
 pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 5793; 455bp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

SQ Sequence 1182 BP; 247 A; 417 C; 361 G; 157 T; 0 U; 0 Other;

Query Match 73.2%; Score 742; DB 11; Length 1182;
 Best Local Similarity 83.9%; Pred. No. 2,6e-119;
 Matches 851; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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QY 169 AAGGAAGTGAAGACGAGACGAGAGCTGGCCAAAGTGTATCTGTGACACCGGCGGACAC 228
DB 169 AAGGAAGTGAAGACGAGACGAGAGCTGGCCAAAGTGTATCTGTGACACCGGCGGACAC 228
QY 61 ATGCGCGGCGCTGGCCGACGCGGCGCAACGCGGCACTACCAAGGCTGCAAGTTGGC 120
DB 229 ATGCGCGGCGCTGGCCGACGCGGCGCAACGCGGCACTACCAAGGCTGCAAGTTGGC 288

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OY 121 GTGCAAGAGTATGTCGCGGCGGAGCTGCGGACCTGCGCAATGTCGCGGCGAG 180
DB 289 GTGCAAGAGTATGTCGCGGCGGAGCTGCGGACCTGCGCAATGTCGCGGCGAG 348
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DB 349 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 408
OY 241 AGCGTGGCGGAGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATG 300
DB 409 ACCGTGGCGGAGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATG 468
OY 301 GACACCTGGAAGAAACCGCTACTTTTGAACCTGCGGAAAGACCGACGACGATC 360
DB 469 GACACCTGGAAGAAACCGCTACTTTTGAACCTGCGGAAAGACCGACGACGATC 528
OY 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 529 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
OY 421 TACAAACCGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATGATG 480
DB 589 TACAAACCGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATGATG 648
OY 481 ATGAAGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 649 ATGAAGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
OY 541 GCGTTCAAGAGCGCTGGGCGGCGCTGGGCGGCGCTGGGCGGCGCTGGGCGGCG 600
DB 709 GCGTTCAAGAGCGCTGGGCGGCGCTGGGCGGCGCTGGGCGGCGCTGGGCGGCG 768
OY 601 CGCGTGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 660
DB 769 CGCGTGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 828
OY 661 CTGCGCGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 829 CTGCGCGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 888
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DB 889 CTGCGGAGAGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 948
OY 781 TCGCGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB 949 GCGCGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1008
OY 841 TCAC---GTCAACAGGCGGCTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 897
DB 1009 TCGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1068
OY 898 GACTGGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 957
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OY 958 ATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
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RESULT 3

ABD07273/c
ABD07273 standard, DNA, 1335 BP.

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XX AC ABD07273;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polynucleotide #5877.
XX XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX KW antibacterial.

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XX OS Pseudomonas aeruginosa.
XX XX
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX XX
XX PF 18-FEB-1999; 99US-00252991.
XX XX
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX DR WPI, 2003-615309/58.
XX DR P-PSDB; ABO73702.
XX XX
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 5877; 455bp; English.
XX XX
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biotech technology. Sequences ABD01397-
XX CC ABD1967 represent P. aeruginosa polynucleotides of the invention. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX XX
XX SQ Sequence 1335 BP; 189 A; 404 C; 485 G; 257 T; 0 U; 0 Other;

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Query Match 73.2%; Score 742; DB 11; Length 1335;
Best Local Similarity 83.9%; Pred. No. 2.6e-119;
Matches 851; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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OY 1 AAGGAAGTGAAGAACGAGAGAGTGGCAAGTGTGATCTGTGGCGACCGGCGGACC 60
DB 1239 AAGGAAGTGAAGAACGAGAGAGTGTGATCTGTGGCGACCGGCGGACC 1180
OY 61 ATGCGCGGCGCTGGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 120
DB 1179 ATGCGCGGCGGCGGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 1120
OY 121 GTGCAAGAGTATGTCGCGGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGG 180
DB 1119 GTGCAAGAGTATGTCGCGGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGG 1060
OY 181 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 1059 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1000
OY 241 AGCGTGGCGGAGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATG 300
DB 999 AGCGTGGCGGAGTGGCGGAGCAATGATGATGATGATGATGATGATGATGATG 940
OY 301 GACACCTGGAAGAAACCGCTACTTTTGAACCTGCGGAAAGACCGACGACGATC 360
DB 939 GACACCTGGAAGAAACCGCTACTTTTGAACCTGCGGAAAGACCGACGACGATC 880
OY 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

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Qy	481	ATGAACGACGAGATTCGATCCGGGCGTGAACGTGAACAAAGTCGATCAATCAAGACGAA	540
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Qy	541	GCTTTCAGAGCGCCCTGGGGCCCGCTGGGCATGTGTGTGTGAAGGCAAGTCTACTGGTTC	600
Db	699	GCCTTTCAGAGCGCCCGTGGGGCCCGCTGGGCATGTGTGTGTGAAGGCAAGTCTACTGGTTC	640
Qy	601	CGCCTGCGGCGCAAGGCGCCACACGGTCACTCCGAGTTTGCACATCAACGATCAGGAGC	660
Db	639	CGGCGACCGGATGAAGCGGCAACAGGTGAATCTCGAGTTTGCACATCAACGATCTCCGG	580
Qy	661	CTGCCCCAGGTGACATCTGCTTACGCTTATGSCAAAGTCAACGACACGGCCTTCAAGGCC	720
Db	579	CTGGCTCCGGTGAATACTCGCTTACGCTTACGCGCAAGTCAAGGACACCGCCTTCAAGGCC	520
Qy	721	CTGGCCACAGAACGGGCGCCAAAGGCGTGAATCATATGCGGCAACCGGCAATAGGCTCGGTGCG	780
Db	519	CTGGCCACAGGCGCGGCGCCAAAGGAGATCATATGCGGCAACCGGCAAGGCTCGGTGCC	460
Qy	781	TCGGGGGTGTGTCAGACCCCTGACGAGACTGCGCAAGAACCGGGGTGCAGATCATTTGTTG	840
Db	459	GCGGGCGTGTGTGCGAACCTTGCAGAGAACTGCCCAAGCAGGGGGGTGCAGATCATCCGCTCC	400
Qy	841	TTCACTCTCAATCCCGGCGGCTTCTGCTCTGCGGCAACGCGAGCAACCGGAGCAAGAAC	897
Db	399	TCGCACTCTCAATCCCGGCGGCTTCTGCTCTGCGGCAACGCGAGCAACCGGAGCAAGAAC	340
Qy	898	GACTGGGTCTGTGCGCCACGACCTTGAACCCGCAAGAGCCCGCATCTTGGCGATGTGGCA	957
Db	339	GACTGGATGTGCGCCACGACCTTGAACCCGCAAGAGCGCGCATCTTGGCGCGGTGCGG	280
Qy	958	ATGACCAAGACCCAGGACAGCAAGGAGCTGTGACGCCATTTTCTGGGAATACTGA	1011
Db	279	ATGACCAAGACCCAGGACAGCAAGGAGCTGTGACGAGATCTTCTGGGAATACTGA	226

XX	RESULT 4
XX	ABD07169
XX	ID ABD07169 standard; DNA; 2748 BP.
XX	ABD07169;
XX	29-JUL-2004 (first entry)
XX	Pseudomonas aeruginosa polymnucleotide #5773.
XX	Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX	antibacterial.
XX	Pseudomonas aeruginosa.
XX	US6551795-B1.
XX	22-APR-2003.
XX	18-FEB-1999; 99US-00252991.
XX	18-FEB-1998; 98US-0074788P.
XX	27-JUL-1998; 98US-0094190P.
XX	(GENO-) GENOME THERAPEUTICS CORP.
XX	Rubenfeld M7, Nolling J, Deloughery C, Bush D;
XX	WPI; 2003-615309/58.

DR P-PSDB; ABO73598 .
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnosis, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX
PS Disclosure; SEQ ID NO 5773; 455bp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnosis,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biotech technology. Sequences ABD0137-
CC ABD1767 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification and was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 2748 BP; 504 A; 1016 C; 870 G; 358 T; 0 U; 0 Other;

Query Match	55.4%	Score 562.2	DB 11	Length 2748
Best Local Similarity	85.2%	Pred. No. 3e-88		
Matches 640	Conservative	0	Mismatches 108	Indels 3
			Gaps	1
QY	264	CAATGACGTGATGTCATGTCATCAACCATGAGCACCGACCTGTGAAAGAAACCGCTA	3233	
Db	1	CGACGACGTGACCGGATGTGATCAACCAAGTATCCGACACCTGTGAAAGAACCGCTA	60	
QY	324	CTTTTGAACCTCTGAGAAAAGACCGACAAACCGATGTGCTGCTTCCATGCGCC	3833	
Db	61	CTTCTCGAACCTCTGCTGAGCAACCGAAMACCTATCTGTGTGTGTGCTGATGCGCC	120	
QY	384	CGGCAACCGCATGTGCGCGCAACCGGCAATGCTGACCTGTACAAACGCGCGTGGCGG	4433	
Db	121	GGGCAACCGGATGTGCGCGCAACCGGATCTCACTGTACAAACGCGCGTGGCGG	180	
QY	444	CAACAGAGACTCGCGGCGCAAGGCGTGTGTGACCAATGACAGAGATTCAGTCCG	5033	
Db	181	CGACAGTGTGCGGACCGGCGGAGGCGTGTGTATCCATGAAACAGACAGATCTTCCG	240	
QY	504	GCGTGAACGTGAGCAAGTGCATCAATCAACCGGAACCTTCAAGCGCGCTGTGGGCC	5633	
Db	241	CCCGACCGGACCAAGATGTCTCATCATMAACCGAAGCGTTCAAGAGCGCGTGGGGCC	3000	
QY	564	GCTGGGCAATGATGTGTGAAAGCAATGCTGATCTGTGTCGCGCTGGCGGCAAGCGSCAC	6233	
Db	301	GCTGGGCAATGATGTGTGAGGAGGAGGAGAGCTACTGTGTCCGCGCACCGGTGAAGCGGACAC	360	
QY	624	GATCACTCCGAGTTGACATCAACAGACAGATCAGACGCTGCGCCGAGGTGACATCGCTA	6833	
Db	361	GATGAACTCCGAGTTGACATCAACAGACATCTCCGCGGTGCTCCGGTGAAGAAATCGCTA	420	
QY	684	CAGCTATGGCAACGTCAACGACACCGGCTTCAAGGCGCTTGGCAACAGAAACGCGCTCAAGGC	7433	
Db	421	CACACTACGGCAACGTCAACGACACCGGCTTCAAGGCGCTTGGCCACAGGCGCGCAAGGC	480	
QY	744	GCTGATCAATGACCGGACCGGCAATGCGTCCGATGCGTGGGATGAGGAGGCGCTGCA	8033	
Db	481	GATCATCAATGACCGGACCGGCAACGCTCCGATGCGTGGGATGAGGAGGCGCTGCA	540	
QY	804	GGAGTGTGCGCAAGAACGCGGTGACAGATCTTGTTCGAC--GTCAACAGGCGGTTT	8600	
Db	541	GGAGTGTGCGCAAGAACGCGGTGACAGATCTTGTTCGAC--GTCAACAGGCGGCTT	6000	
QY	861	CGTGTGCGTAAACCGGACAGCCGACGACAGACATCTGGGTCTGTGGCTTCAACACTT	9220	

Db 601 CGTCTGCGCAACGCCGAGACGCCGAGACGACGATGATGTCGCCACGACCT 660
QY 921 GAACCCGAGAAAGCCCGCATCTGTCGATGTCGATGACCAAGCCAGACGAA 980
Db 661 GAACCCGAGAAAGCCCGCATCTGTCGATGTCGATGACCAAGCCAGACGAA 720
QY 981 GGAGCTGCAAGCGCATTTTCTGAGATCTGA 1011
Db 721 GGAGCTGCAAGCGCATTTTCTGAGATCTGA 751

RESULT 5

AA043365
ID AA043365 standard; DNA; 300 BP.

XX AA043365;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 13-OCT-1993 (first entry)
XX Pseudomonas 7A glutaminase N-terminus coding region.
XX Neoplasm; glutamine; anticancer; antiviral; therapy;
KW Pseudomonas 7A-Glutaminase-Asparaginase; PGA; ss.
XX Pseudomonas .sp. 7A.

XX Key Location/Qualifiers
FH mat_peptide 1..300

FT /note= "corresponds to first 100 amino acids at mature N-terminus of enzyme"
FT 200..201
FT /*tag= b
FT /*note= "not identified"

XX DE4140003-A1.

XX 09-JUN-1993.

XX 04-DEC-1991; 91DE-04140003.

XX 04-DEC-1991; 91DE-04140003.

XX (ROBE/) ROBERTS J.

XX Roberts J.

XX WPI; 1993-189322/24.

XX P-PSDB; AAR37660.

XX DNA encoding low mol.wt. glutaminase - used for glutamine isolation from human tissues or fluids for treating cancer and HIV.

XX Claim 5; Fig 1; 16pp; German.

XX A gene library was prepared from Sau3A-digested chromosomal DNA of Pseudomonas 7A (ATCC 29598). Three oligonucleotide probes were synthesized based on amino acid sequences of peptide fragments from the N-terminus, middle and C-terminus of the mature glutaminase (see AA043362-Q43364, respectively). A single clone hybridized to all three probes. CC Further analysis resulted in isolation of a 1.1kb SalI fragment which encoded a 23 amino acid signal peptide and some of the N-terminal amino acids of the mature protein. Sequence AA043365 starts from the mature N-terminus of the glutaminase. The enzyme will be potentially useful in CC anti-tumor therapy in neoplastic tissues where glutamine levels are often increased. (Updated on 25-MAR-2003 to correct PN field.) (Updated CC on 24-OCT-2003 to standardise OS field)

XX Sequence 300 BP; 66 A; 95 C; 97 G; 40 T; 0 U; 2 Other;

Query Match 27.7%; Score 281; DB 2; Length 300;

Best Local Similarity 96.0%; Pred. No. 1.3e-39;
Matches 287; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGAAAGTGAAGAACACAGACAGAGTGGCAACGTGTGTATCTTGGCCACCGCGGCAAC 60
Db 1 AAGAAAGTGAAGAACACAGACAGAGTGGCAACGTGTGTATCTTGGCCACCGCGGCAAC 60
QY 61 ATCCGCGCGCTGGGCGCGGCGGCGCAAGCGGCACTTACAGAGCTGCGCAAGTGGAC 120
Db 61 ATCCGCGCGCTGGGCGCGGCGGCGCAAGCGGCACTTACAGAGCTGCGCAAGTGGAC 120
QY 121 GTCCAGAAAGTGAATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 121 GTCCAGAAAGTGAATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 CAGGTGATGACAGATGCTCCGAAAGCATCACCAACGACGACCTGCTCAAGTGGCAAGC 240
Db 181 CAGGTGATGACAGATGCTCCGAAAGCATCACCAACGACGACCTGCTCAAGTGGCAAGC 240
QY 241 AGCGTGGCGGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299
Db 241 AGCGTGGCGGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299

RESULT 6

ADA31049
ID ADA31049 standard; DNA; 1125 BP.

XX ADA31049;

XX 20-NOV-2003 (first entry)

XX DNA encoding Acinetobacter baumannii protein #2336.

XX de; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
KW vaccine; plant biocontrol agent.

XX Acinetobacter baumannii.

XX US6562958-B1.

XX 13-MAY-2003.

XX 04-JUN-1999; 99US-00328352.

XX 09-JUN-1998; 98US-0086701P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton G, Bush D;

XX WPI; 2003-576092/54.

XX P-PSDB; ADA35175.

XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.

XX Example; SEQ ID NO 2336; 328bp; English.

XX The invention relates to isolated Acinetobacter baumannii nucleic acids. CC The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species, in a sample, in screening CC compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for CC plants. The present sequence represents DNA encoding an A. baumannii protein.

XX Sequence 1125 BP; 333 A; 224 C; 223 G; 345 T; 0 U; 0 Other;

Query Match 26.9%; Score 273; DB 9; Length 1125;
 Best Local Similarity 56.2%; Pred. No. 3e-38;
 Matches 557; Conservative 0; Mismatches 425; Indels 9; Gaps 2;

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QY 30 CAAGTGTGATCTCTGGCCACCGGCGACATCGCCGCGCTGGCCGACGCGGCCAA 89
DB 135 CAATGTGTGTGTGTGCTGCTACTGGCGGTACATGTCTGTCTGCGCAACTCAGCAAA 194
QY 90 CAGGCGCCACTACCAAGGCTGCGCAAGGTGGCGTCGACCAAGCTGATTTGGCGCGTCCGA 149
DB 195 TAGTGCAACTTATACGGCGGCAAAAGTTCCAGTTGATGCTTTATCATGACAGTTTCTCA 254
QY 150 GCTGCGCGACCTGGCCAAATGTGCGCGCGACGAGAGGTATGCAAGATCGCTCCGAAAGCAT 209
DB 255 AATTCAAGATTGTGGCAATGTATCTGTATCCAGCATTAAGAAGTCTCTGAAAGTAT 314
QY 210 CACCAAGAGACCTGCTCAAGCTGCGCAAGAGAGGTGGCCGAGCTGGCGCGACAGCAATGA 269
DB 315 TACTGACAAAGAAATTAATTAACAATTTGCTGCAAGTAATGAACCTGTTAAAAAGCCAA 374
QY 270 CGTGGATGGCATTCGTCAATCCATGGCACCGACACCTGGAGAAACCGGCTACTTTT 329
DB 375 TGTAAATGCGCTTGATTAACAACGGTACAGATTAATTAAAGAAACAGATTTTCTT 434
QY 330 GAACCTCGTGAAGAAACCGACCAAGCGATGCTGTGCTGCTTCATGCGCCCGGCGAC 389
DB 435 AATCTGTGTCTCACTGATTAACCAATGTAATCTGTGGCTCAATGCGCCCATCAAC 494
QY 390 CGGCATGCGCCGCGACCGGCAATGCTCAACCTGTACAAAGCGCGTGGCGCGGCGACGACAA 449
DB 495 TGCCTTTTCACAGATGTGTCACTTAACCTTTATAGTCTGTGATGTGCGCGCTTCTGA 554
QY 450 GGACTCGCGCGGCAAGGCGGTGCTGTGACCATGACGACGACGATCCAGTCCGGCGGTGA 509
DB 555 TGAATGCAAAAATTAAGCGCTTATGTGTCTCATGAACAATCTTTTGTGCTCGTGA 614
QY 510 CGTGAAGCATGTCATCAATCAAGACCGAACTTCAAGAGCGCTGGCGCGCTGGG 569
DB 615 TGTAACTTAAGGCAATTAATTCATTAACAATGCTTTTGAAGCCAAATGGGCTGCTTGGG 674
QY 570 CATGCTGTGGAAGGCAAGGTGTAATGCTGTGCGGCTGCGCGGCAAGCGCCACAGGTGAA 629
DB 675 TACCTGTGTGAAGGCAACCAATGTGTTAGAACATCTGTTAAAGTCAATCAATGC 734
QY 630 CTCCGAGTTCCACATCAAGATCAGCAGC-----CTGCCCGAGGTGACATCGCCTA 683
DB 735 TTCAGAATTTAATTAATTAAGTAAATTAAGTGAATGCTTCCGACAGTAAATCGTTTA 794
QY 684 CAGCTATGGAAGTCAACGACGACGCGCTTACAGGCGCTTGGACAGAAAGCGCGCAAGGC 743
DB 795 TGGTTCGTGACTCTATGCTTCTGTGATGCTTAAGACATATGCAAAAGCTGCGCTAAAGC 854
QY 744 GCTATCATGCGCGGCAAGGCAATGCTGCTGTGCTGCGGCGGCGGCGGCGGCGGCGCA 803
DB 855 GATTATTCATGAGGTATGAGGTATGCTTGTGAGCGAAATATATCGTTCAACATTTACA 914
QY 804 GGAAGCTGC---GCAAGAACGCGGTGACATGATCTGTTGTCACGTCACAGCGCGGTTT 860
DB 915 AAACCTTCATGACAAAACGGAATTCATTAATTCGCTCATCGCGCTTCCACAGGTTT 974
QY 861 CGTGCTGTGTAACCGCGACGAGCGCGACGACGACGACGACGACGAGTGGTCTGCGCCACGACT 920
DB 975 TGTATTAAGTATGACGAGAACCTGATCTTAATATATGTTGGGTAGGAGCTCATGATTT 1034
QY 921 GAACCCGAGAAAGCGCGCATCTTGGCGATGTGGCATGACAAAGACCGGACGACGAA 980
DB 1035 GAATCTCTAAAGAGGCGCTTCTTGGCGCGTGGCACTTACAAAGCAACGATGCGAA 1094
QY 981 GGAGCTGACGCGATTTTCTGGGAATCTGA 1011
DB 1095 AGAATTCACGCAATGTTCTGGCAGTACTAA 1125

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RESULT 7
 AANT0557
 ID AANT0557 standard; DNA; 2837 BP.

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XX AC AANT0557;
XX AC 25-MAR-2003 (revised)
DT 07-AUG-1991 (first entry)
XX DE Sequence encoding a protein with L-asparaginase (LA) activity in pASN 30
or pASN 32.
XX KM Enzyme; cancer therapy; leukemia therapy; ss.
XX OS Erwinia chrysanthemi.
XX FH Key Location/Qualifiers
FT misc_feature 1..25
FT /*tag= a
FT /label= pUC9 linker
FT sig_peptide 61..723
FT /*tag= b
FT mat_peptide 724..1707
FT /*tag= c
FT /*note= "claimed"
FT terminator 172..1789
FT /*tag= d
XX PN EP211639-A.
XX PD 25-FEB-1987.
XX PF 04-AUG-1986; 86EP-00305984.
XX PR 06-AUG-1985; 85GB-00019753.
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Minton NP, Gilbert HJ;
XX DR WPI: 1987-051784/08.
XX DR P-PSDB; MAP70348.
XX PT New recombinant plasmids coding for L-asparaginase - esp. from Erwinia
carotovora, useful for treating malignancies and new transformed hosts.
XX PS Disclosure; Fig 4; 35pp; English.
XX CC When E. carotovora SGR1 193 contg. plasmid pASN 32 was cultured, the cell-
CC free culture broth contained 11.19 LA units/ml with specific activity
CC 53.34 units/mg of protein. These figures compare with 10.87 LA units/ml
CC and 14.97 units/mg of protein for the currently used prodn. strain
CC E. chrysanthemi NCPB 1066. (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 2837 BP; 627 A; 665 C; 867 G; 678 T; 0 U; 0 Other;

Query Match 25.8%; Score 261.6; DB 1; Length 2837;
Best Local Similarity 55.6%; Pred. No. 2.7e-36;
Matches 554; Conservative 0; Mismatches 424; Indels 18; Gaps 2;

QY 20 AGAAGTGGGCAACGTGTATCTTGGCCACCGGCGGACCATGCGCGGCTGGCGGCA 79
DB 728 ATAAAGTCCCAATATGTTATCTGTGCGACCGGCGGTACAAATTTGCCGCTCACGGCA 787
QY 80 GCGGCGGCAACAGCGCACTTACAGGCTGCGCAAGTTGGGTGTCGACAGTGAATGGCG 139
DB 788 CGGGTACCAACCAACGATTAACAGGCTGCGCGCTTGGGTGATACGTTAATCAACG 847
QY 140 GCGTCCGGAAGTGGCGGACCTGCGCAATGTGCGCGCGGACGAGTATGACATGCGCT 199
DB 848 CTGTGCTGTGATGAAGAACTGGCTTAATGTGAAGGGGAGCACTTCTCCAAATGCGCA 907
QY 200 CCGAAGCATCACCAACGACGAGCTGCTCAAGCTGGCAAGCAGCGTGGCGGCTGGCGG 259

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QY 626 TCAACTCCGAGTTCCGACATCAAGCAGATGACGAGCCCTGCCCCAGGTGACATCGCCTTACA 685
 DB 662 GCGATACGCGCATTCGATGCTCTAAGCTGAATGAGTCCGAAAGTCCGATCGTTTATA 721
 QY 686 GGTATGCGCACTGACACGAGCTTACAAAGGCTTGGCAAGAACGCGCGCAAGGCGC 745
 DB 722 ACTACGCTAACGCAATCCGATCTTCCGCTTAAAGCACTGGTAAATGCGGCTATGATGCA 781
 QY 746 TGATCCATCCCGGCAACCGGCAATGCTCGGTGCTCGGGGTGTCAGCCCTGCAAG 805
 DB 782 TCGTTAGCGCTGCTGTGCTGTAATGTAACCTGTATTAATCCGTTTCCACACCTCGGCA 841
 QY 806 AGCTGCGCAAGAACGCGCTGACGATCATCTTCTGCTACGCTCAACAGGCGGCTTGTGTC 865
 DB 842 CGCGCGCGAAAGAACGCGCATGCAAGTACGCTGCTTCCCGGCTAACCGAGCGGTGCTACCA 901
 QY 866 TCGGTACCGCCGACGAGCCCGGACGACAAAGACCTGGGTCTGGGCCCAACCTGTAAC 925
 DB 902 CTGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 961
 QY 926 CGCAGAAAGCGCGCATCTGCGCATGCTGCGCATGCTGCGCATGCTGCGCATGCTGCGCAT 985
 DB 962 CGCAGAAAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021
 QY 986 TCGAGCGCATTTTCTGGAATAC 1008
 DB 1022 TCCAGCAGATCTTCAATCAGTAC 1044

RESULT 9
 AAT96346
 ID AAT96346 standard; cDNA; 1848 BP.
 AC AAT96346;

DT 08-APR-1998 (first entry)

XX Chimeric gene containing anti-asparaginase MAb light and heavy chain.

DE Immunoglobulin Ig; heavy chain; variable region; murine; human;

KW asparaginase II; monoclonal antibody; MAb; light chain;

KM recombinant chimeric polypeptide; ss.

XX Synthetic.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX US5686579-A.

XX 11-NOV-1997.

XX 23-MAY-1995; 95US-00447422.

XX 21-JUN-1988; 88US-00205748.

XX 31-AUG-1992; 92US-00938505.

XX 22-JUN-1993; 93US-00081410.

XX (HYBR-) HYBRISENS LTD.

XX Rothstein A, Ramjeesingh M, Shaml EX;

XX WPI; 1997-558200/51.

XX Self-protecting chimeric polypeptide comprising biologically active

XX sequence and single-chain antibody sequence - has resistance to e.g.

XX disrupting temperature, presence of proteolytic enzymes, etc.

Example 2; Col 27-30; 29pp; English.

The present sequence is a chimeric gene containing the cDNA for the
 CC immunoglobulin (Ig) heavy and light chain variable regions of a murine
 CC anti-asparaginase II monoclonal antibody (MAb), and human asparaginase

CC II. The gene was used in the preparation of a novel recombinant chimeric
 CC polypeptide, comprising a 1st region comprising a biologically active
 CC domain and another domain containing an epitope, linked via a polypeptide
 CC to a 2nd region including a single chain antibody (SCA) having the light
 CC and heavy chains of an antibody variable region which specifically binds
 CC the epitope in the 1st region. The chimeric polypeptide assumes a
 CC conformation in which the SCA is bound to the epitope of the 1st region
 CC and protects its biological activity from deactivation by denaturing
 CC temperatures or pH conditions, proteolytic enzymes, oxidizing agents or
 CC alcohol. The regions of the chimeric polypeptide interact to form a
 CC structure analogous to an antibody-antigen complex. A L-asparaginase-SCA
 CC fusion protein of the above type has better trypsin resistance than free
 CC L-asparaginase

SQ Sequence 1848 BP; 435 A; 498 C; 517 G; 398 T; 0 U; 0 Other;

Query Match 23.7%; Score 240.8; DB 2; Length 1848;
 Best Local Similarity 55.0%; Pred. No. 1.1e-32;
 Matches 542; Conservative 0; Mismatches 432; Indels 12; Gaps 3;

QY 29 CCAAGCTGATCTCTGCGCAACCGCGGCAACCATGCGCGGCTGCGCGGCGCA 88
 DB 872 CCAATATCACCATTTTACCAACCGCGGACCATTTGCGGTGATCTCGCAACA 931
 QY 89 ACAGCGCACTTACAGGCTGCAAGTTGCGGTGCAAGCTGATTCGCGGCTGCGG 148
 DB 932 A---ATCTACTACACAGTGGGTAAAGTTGGCGTAAGAAATCTGTTAATGCGGCGCG 988
 QY 149 AGCTGCGGACCTGCGCAATGCGCGGCGGAGAGGTGATGATGATGATGATGATGATGATGAT 208
 DB 989 AACTTAAAGACATTCGCAAGCTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
 QY 209 TCACCAACGACGACCTGCTCAAGCTGCGCAAGCGGTGCGGAGCTGCGGCGCAAGCAATG 268
 DB 1049 TGAAGATTAATGTCTGCTGACACCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102
 QY 269 AGCTGATGCGATGCTATCAACCCATGCGACCGACCCCTGGAAGAAACCGCTTACTTT 328
 DB 1103 AGACCGAGCGGCTTCTGCTATTAACCGGCTACCGACCATGAGAGAACTGTTACTTCC 1162
 QY 329 TGAACCTGCTGAAAG 388
 DB 1163 TCGACCTTACAGGTGAATGCAACCAACCGGTGATGATGATGATGATGATGATGATGATGAT 1222
 QY 389 CCGCATGCTCGCGCAGCGCATGCTCAACCTGTAACAGCGGCTGCGGCGCAACA 448
 DB 1223 CGCTATGAGGCGAGAGCTGCTCAACCTGTAACAGCGGCTGCGGCGCAACA 1282
 QY 449 AGAAGCTGCGCGGCGAGAGGCTGCTGATGACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 508
 DB 1283 AAGCTCGCGCAACCGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1342
 QY 509 ACGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
 DB 1343 ACGTACCAAAACCAACCAACCGAGTGAAGCACTTCAAGCTGTTAACTAGGCTCTC 1402
 QY 566 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
 DB 1403 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1462
 QY 626 TCAACTCCGAGTTGCAATCAAGCAGATGACGAGCTTCCCAAGGTGACATCGCTTACA 685
 DB 1463 GCGACACGCGCATTCGATGCTCTAAGCTGAATGAATCCCAAGTCCGAGATTTGTTTATA 1522
 QY 686 GGTATGAGCAAGTCAACGAGCGCTTCAAGGCGCTTGGCAAGAGCGGCGCAAGGCGC 745
 DB 1523 ACTAAGCTTACGATCGATCTTCCGCTTAAAGCACTGTAAGATGCGGCTATGATGCA 1582
 QY 746 TGATCCATGCGGCAACCGGCAATGCTGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCGG 805
 DB 1583 TCGTTAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1642
 QY 806 AGCTGCGCAAGAACGCGCGTGAAGATCATCTTCTGCTACGCTCAACAGGCGGCTTGTGTC 865

KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM covalent modification; acylation; pharmacokinetic; immunogenic; spleen;
 KM hypersensitive; reduced toxicity; immunosuppression; allergy; thymus;
 XX lymphocyte marker distribution; hepatotoxicity; ss.

OS Wolinella succinogenes.

PN WO9856410-A1.

PD 17-DEC-1996.

XX 09-JUN-1998; 98WO-US011905.

XX 09-JUN-1997; 97US-0049085P.

XX (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.

XX Durden DL;

XX WPI; 1999-070295/06.

XX Treating diseases responsive to asparagine depletion - especially cancer
 PT and auto-immune diseases, using a Wolinella succinogenes asparaginase.

XX Example 5; Fig 6; 58pp; English.

XX This sequence is a novel L-asparaginase gene from Wolinella succinogenes
 CC which is used in a method for the treatment of diseases that respond to
 CC asparagine depletion. This asparaginase and its analogues, are
 CC particularly used to treat (i) malignant diseases, particularly where
 CC haematological and acute phases) and (ii) autoimmune diseases,
 CC either chronic or acute phases) and (iii) autoimmune diseases,
 CC specifically rheumatoid arthritis, systemic lupus erythematosus and
 CC acquired immune deficiency syndrome, in humans or other mammals. The
 CC asparaginase can also be used for the covalent modification of
 CC biologically active proteins by acylation which is used to alter
 CC pharmacokinetic and immunogenic properties of biologically active
 CC proteins, and can be applied to any protein used to treat animal, human
 CC or plant diseases. The asparaginase can be used to treat patients who
 CC have become hypersensitive to other microbial asparaginases. The
 CC asparaginase has reduced toxicity and reduced tendency to cause
 CC immunosuppression or allergy, particularly it has no effect on spleen and
 CC thymus histology or lymphocyte marker distribution and no hepatotoxicity
 CC
 SQ Sequence 1133 BP; 315 A; 305 C; 267 G; 246 T; 0 U; 0 Other;

Query Match 21.6%; Score 219; DB 2; Length 1133;

Best Local Similarity 52.8%; Pred. No. 6,4e-29;

Matches 521; Conservative 0; Mismatches 460; Indels 6; Gaps 2;

QY 29 CCNAACGTGTGATCTGTGGCCAGCGGCGGACCATCCCGCGCTGGCGCCAGCGCGCCA 88
 DB 128 CCCAAGTGAATCTTCCAGCAGCAGGAGGACCATCGCTGGCGGGAATCAGGTCA 187
 QY 89 ACAGCGCCACTTACCAAGGCTGCCAAGCTTGGCTGCAAGCTAATGGCGGCTGCCG 148
 DB 188 AAGAG--TAGTACTCTGCTGAGAGCAGTCAACGCTTATTAAGCTTCTTGACGCGTCC 244
 QY 149 AGCTGCGCCAGCTGGCGCAATGTCGCGGAGAGAGAGTATGCAAGTCGCTCCGAAAGA 208
 DB 245 CCATCAACCACTTACGACCATCAAGGAGGAGAAAGTTCAGACATTTGCTCCCAAGAGA 304
 QY 209 TCACCAACGACGACCTGTCAAGCTGGCAAGCAGCTGGCCGAGCTGCCAGCAATG 268
 DB 305 TGAACGGTAAAGTGTGGCTTAACTAGCCAGGCTGTCAATAGCTCCTCCGCCAAGAG 364
 QY 269 AGGTGATGGCATCTCATCAACCATGCAACCGACCTCTGAAAGAACCGCTACTTTT 328
 DB 365 AAGACGAAACCGGATCATCAACCATGCAACCGACCTCTGAAAGAACCGCTACTTTT 424
 QY 329 TGAACCTCTGTGAAAGAACCGACCAACCGATGCTGTGCTGCTTCAAGCGCCCGGCA 388
 DB 425 TCAACCTCAAGGTGAAAGAACCGACCAACCGATGCTGTGCTGCTTCAAGCGCCCGGCT 484

QY 389 CGCCATGTCGCGGACGCGATGCTCAACCTGTACCAAGCGCTGGCCGTGCGCACACA 448
 DB 485 CTTCAATAGTGTGATGGCCCCCATGAATCTTAAAGCGCGTGAATAGCATCAACA 544
 QY 449 AGAATCGCGGGGCAAGGCGCTGTGTGACCAATGAAGAAGATTCAGTCCGGGCGT 508
 DB 545 AAGCTCTTACTTAAACAAAGAGTGTGATTTGATGAAGATGATGATCAACGCGCAAG 604
 QY 509 AGTGAAGATGATGATCAACATCAAGACCGAGCTTCA--GAGCGCTGGGCGCCGC 565
 DB 605 AAGGACCAAGCTCAACACACCGAGTCAATGATTTGCTTGGCCCAACAGGTAAAG 664
 QY 566 TGGCATGTGTGAGAGCAAGTGTGATCTGCTTCCGCTCGCGGCAAGCGCCACAG 625
 DB 665 TCGGACAGTCTAATATGCAAGAGTGAATTTCACTCAATCCGTTGACCTCACACC 724
 QY 626 TCAACTCCGATTTGACATCAAGCAAGATACAGACGCTGCGGAGTGAATCGCTCA 685
 DB 725 TTGCAAGTGAATTTGATTTTGAACAAATGCAAGAACTCCAGAGTGAATTTCTTACG 784
 QY 686 GCTATGCAAGCTCAACGACGCGCTCAAGGCGCTGGCACAGACGCGCCAGAGCGC 745
 DB 785 CTCACCCGATGATGATCTGATTTTATGCAATGACGCGCTTCAAGCAGAGCCAAAGAA 844
 QY 746 TGATTCATGCGCGCACCGGCAATGGCTGCTGCTGCTGCGGAGTGTGCAAGCTTCAAG 805
 DB 845 TCATTCATGACGAGCATGGGCAATGGGAACCTTTCCCTTTCATCAATGCTCTTGAAA 904
 QY 806 AGTGGCGAAGAACGCGCTGCAAGATCATTTGCTGTCAACGTCAACAGGCGGTTGCGT 865
 DB 905 AAGCAGCCAAATCAAGGCGCTGATGCTGCTGCAAGCTTGAAGTGGGAGTGTTCACCA 964
 QY 866 TGGTAAAGCGGAGAGCGCCGACGACAGAAAGACTGGGTGCGGCGCCACGATGAACC 925
 DB 965 CCCAAGAGGCTGAAGTGAATGATGAAGAACTTGTGTTGTGGCTACAGAGTCTCAACC 1024
 QY 926 CGCAGAGAGCGCGCATCTGTGCGATGTGGCAATGACCAAGACCGAGACAGAAAGAGC 985
 DB 1025 CTCAAAAAGCAGAGTGTCTTATGTTAAGCCCTCACCAAAACTGATATGAGAGGCGA 1084
 QY 986 TGCAGCGCATTTTCGGGAATATGAT 1012
 DB 1085 TCCAAAAGATCTTCTCACTTATAT 1111

RESULT 12

AAC62512

ID AAC62512 standard; DNA; 1133 BP.

XX AAC62512;

XX 07-FEB-2001 (first entry)

XX W. succinogenes asparaginase-specific DNA insert.

XX Asparaginase; glutaminase; autoimmune disease; graft versus host disease;
 KM leukaemia; DNA insert; ds.

XX Wolinella succinogenes.

OS WO200059533-A1.

PN 12-OCT-2000.

PD 24-MAR-2000; 2000WO-US007981.

XX 02-APR-1999; 99US-0127662P.

XX (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.

XX Durden DL;

DR WPI; 2000-664963/64.

XX Treating or preventing graft versus host and autoimmune diseases, e.g.
PT diabetes, rheumatoid arthritis, that responds to asparagine or glutamine
PT depletion comprises administering an asparaginase or glutaminase.

PS Example 5; Fig 6; 72pp; English.

XX The present invention relates to a novel method of using the recombinant
CC microbial enzymes asparaginase and glutaminase to treat autoimmune
CC diseases and leukemia. The diseases likely to respond to such treatment
CC include graft versus host disease, rheumatoid arthritis, systemic lupus
CC erythematosus, autoimmune hemolytic anemia, collagen vascular diseases, AIDS,
CC osteoarthritis, Isaac's syndrome, psoriasis, diabetes, multiple
CC sclerosis, sclerosing pancreatitis, rheumatic fever, inflammatory
CC bowel diseases, primary biliary cirrhosis, chronic active hepatitis,
CC glomerulonephritis, myasthenia gravis, pemphigus vulgaris and Graves
CC disease. The present sequence is DNA insert used to demonstrate the
CC method of the invention

80 Sequence 1133 BP, 315 A, 305 C, 267 G, 246 T, 0 U, 0 Other;

Query Match 21.6%; Score 219; DB 3; Length 1133;

Best Local Similarity 52.8%; Pred. No. 6.4e-29;

Matches 521; Conservative 0; Mismatches 460; Indels 6; Gaps 2;

QY 29 CCAACGTGTGATCTCTGCGCCACCGGCGGACCATCCCGCGCTGGCGGCGGCGCA 88
DB 128 CCCAAGTGTACTCTCTGCGCCACCGGCGGACCATCCCGCGCTGGCGGCGGCGCA 187
QY 89 ACAGCGCCACCTTACAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 148
DB 188 AAGG---TAGTACTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244
QY 149 AGCTGGCCGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 208
DB 245 CCATCAACGACCTTACAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 304
QY 209 TCACCAACGACCTTACAGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 268
DB 305 TACCGGCTGAGGTGTGCTTAACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364
QY 269 AGCTGTGATGATCTCTGCGCCACCGGCGGACCATCCCGCGCTGGCGGCGGCGCA 328
DB 365 AAGCGAAGCGGCTGATCATCACTGATGATCACTGATGATGATGATGATGATGAT 424
QY 329 TGAACCTGTGAAAAAGACCGACGACGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 388
DB 425 TCAACCTGACGGTGAAGAAAGCAAAACCTGTGCTGTGCTGTGCTGTGCTGTGCTG 484
QY 389 CGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 448
DB 485 CTTCATGTGATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 544
QY 449 AGGACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 508
DB 545 AAGCTCTTCTAACAAGAGGTGTGATGTGATGATGATGATGATGATGATGATGATG 604
QY 509 AGGTGACGATGTGATCAATCAAGACCGACCTTCAA--GAGCGCTGGGCGGCGGCG 565
DB 605 AAGCGACGACGCTCAACCAACCGGCTGATGATGATGATGATGATGATGATGATGAT 664
QY 566 TGGGCTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 625
DB 665 TGGGCTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 724
QY 626 TGAACCTCGGCTGTGATCAATCAAGACCGACCTTCAA--GAGCGCTGGGCGGCGGCG 685
DB 725 TTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784
QY 686 GGTATGCGCAAGTCAACCGGCGGCTTACAGGCGGCTTGGCGGCGGCGGCGGCGGCGG 745
DB 785 CTCACCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 844

QY 746 TGATCATGCGGCAACCGGCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 805
DB 845 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
QY 806 AGCTGTGCAAGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 865
DB 905 AAGCGACGACGCTCAACCAACCGGCTGATGATGATGATGATGATGATGATGATGATG 964
QY 866 TGGGCTGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 925
DB 965 CCCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1024
QY 926 CGGAGAGGCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 985
DB 1025 CTCGAGAGGCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1084
QY 986 TGCAGGCGATTTCTGGAATCTGAT 1012
DB 1085 TCCGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1111

RESULT 13

ABZ80801

ID ABZ80801 standard; DNA, 1174 BP.

XX

XX ABZ80801;

XX

XX 27-OCT-2003 (revised)

XX 30-MAY-2003 (first entry)

XX

XX Erwinia carotovora L-asparaginase gene.

XX

XX gene; de; asparaginase; cytostatic; blood; acute lymphoblastic leukemia.

XX

XX Pectobacterium carotovorum.

XX

XX Key Location/Qualifiers

XX CDS 48..1094

XX /tag= a

XX /product= "L-asparaginase"

XX /EC_number= "3.5.1.1"

XX primer_bind 48..72

XX /tag= b

XX /bound_molecly= "primer N204"

XX /tag= c

XX /bound_molecly= "primer C204"

XX

XX MO2003018742-A2.

XX

XX 06-MAR-2003.

XX

XX 21-AUG-2002; 2002WC-RU000405.

XX

XX 22-AUG-2001; 2001RU-00123442.

XX

XX 04-APR-2002; 2002RU-00108505.

XX

XX (UCHR=) GOS UCHREZHENIE NI INST BIOMED KHMII.

XX (UCHR=) GOS UCHREZHENIE TSENTR BIOINZHENIYA.

XX

XX Eldarov MA, Zhgun AA, Geraziev YV, Aleksandrova SS, Bogush VG;

XX Sidoruk KV, Sveshnikova EV, Borisova AA, Omeinyuk NV, Archakov AI;

XX Skryabin KG, Sokolov NN;

XX

XX WPI; 2003-268418/26.

XX P-PSDB; ABP98615.

XX

XX New isolated Erwinia carotovora L-asparaginase gene useful for producing

XX a L-asparaginase protein useful for treating malignant and nonmalignant

XX diseases of the blood.

XX

XX Claim 2; Page 22-23; 29pp; Russian.

XX This sequence represents a DNA fragment coding for an *Erwinia carotovora*
 CC L-asparaginase. The invention also includes a homogeneous preparation of
 CC a mature form of L-asparaginase produced by expression of the DNA in a
 CC bacterial strain and has low affinity for L-glutamine. The L-asparaginase
 CC protein encoded by the DNA is useful for treating malignant and non-
 CC malignant diseases of the blood (e.g. acute lymphoblastic leukemia).
 CC (Updated on 27-Oct-2003 to standardise OS field)

XX Sequence 1174 BP; 290 A; 284 C; 313 G; 287 T; 0 U; 0 Other;

Query Match 20.6%; Score 209.2; DB 8; Length 1174;
 Best Local Similarity 54.1%; Pred. No. 3.2e-27;
 Matches 471; Conservative 0; Mismatches 393; Indels 6; Gaps 2;

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20  AAGAGTGGGCAACGCTGATCTCTGACACCGGCGACCAATCGCGGCGGCGCA 79
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118  AAAATCTACTTACCTATTCATTCTGCAACAGCGCGTTCGATTGCCGATTGCA 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
80  GCGCGGCAACAGCGGCACTTACAGCTGCGCAAGTTGGCGTGCACAGTATTGCGG 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178  GCCAATACGCAACCACTGGTAAAGCGGTCGCGCGTGAAGAGACGTGATTCAAG 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
140  GCGTGGCGGAGCTGGCGGCACTGGCCATATGTGCGCGGCAAGAGTATGATGCTT 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
238  CGGTGCTGAGCTGAAGAGCTTGCCTGCAATATCAAGGTAGACAGTTGCGACATCGCA 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
200  CCGAAGACATCAACCAAGACAGCTGCTCAAGCTGGCAAGACGTTGGCGAGCTGGCCG 259
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
298  GTGAAAATATGACAGCGCATGTGTTTAAAGCTGAGCAGAGCGGTGAACGAGCTGCTG 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
260  ACAGCAATGACGTCATGATGCTGATCATCAACCATGACCGACACCTGGAAGAAACCG 319
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
358  CAGCGACGATGTGATGCGTGTGATTAACGACGATGCGATACGCTGACGATCTC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
320  CCTACTTTTGAACCTCGTGGAAAAAGACGACAGCCATCGTGGTGGTCTCATGCG 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
418  CTTATTTTCTGAACCTGACGCTGAAAGGACAGCAAGCACTTCTTTTGCATATGCGTCCG 477
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380  GCCCGGCAACCGCATGTCCGCGACAGCGGATGCTCAACCTGTACCAACGCGGTCGCGTGG 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
478  GCAAGGCAATCAAGT---CCGACGCGCCCATGAACTGTATCGGTGCAATGAAAGTGG 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
440  CCAGCAACAAAGACTCGCGCGGCAAGGCGCTGTGTGACATGAACGACGATCCAGT 499
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
535  CAGCGATTAATACTCCGCGGTCGGGTGATGCTGTGCTGAACGACCGCATTTGGTT 594
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
500  CCGGCGCTGACGTGACAGTGTGATCAATCAAGACCGAAGCTTTCA---GAGCGCT 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
595  CTGCCCGTTTCACTAGCAAAACCAACGCTTTAAGTTGATACCTTTAAAGCGCCAGAG 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
557  GGGGCGCGCTGGCATGTGTGTGAAGGACGATGCTGTTCGCGCTGCGGCGCAAGC 616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
655  AAGGTTATTTGGGCGGATTAATCGGTGAACAAATATCTACACAGCCGCTGTGATTAAG 714
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
617  GCCACACGCTCACTCCGAGTTTGAACATCAAGACATGACAGCTGCCCGAGGTGACA 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
715  TTCACACCAACGCGTTCGTTGTTGATGACCAAGTTGATAGCTGCGGAAGTGCACA 774
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
677  TGGCTTACGCTATGAGCACTGACCGGACCGGCTTACAGGCGCTTGGGACAGAAACGGGG 736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
775  TTATTTATGTTATACGAGACGATTCAGAAATATATGATATACCTCTTATCAAAACGGGG 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
737  CCAAGGCGCTGATCACTGCGGCAACCGGCAATGCTCGGTGCTGTCGCGGCTGTGTCAG 796
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835  TAAAGGATCTGTATGTCGGGCAATGTCGAGGCAAGCTATTCAGAGCGGCGACGCTG 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
797  CCTGTGAGAGCTGCGCAAGAACGCGGTGACAGATCACTTGTGCTACGCTCAACAGGGCG 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
895  GCATCCGTAAACGGAACCAAGGCAATGTTGTGTGATGCTTCCAGCGTACCGGACGGG 954
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
857  GTTTCGTGTGCTAAGCGGCAAGCCCG 886
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 955 GTATCTCCACCGGATGACAGGCCAACCCG 984

RESULT 14

ABD07233/C

ID ABD07233 standard; DNA, 270 BP.

AC ABD07233;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #5837.

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;

KW antibacterial.

OS Pseudomonas aeruginosa.

PN US651795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

DR WPI; 2003-615309/58.

DR P-PsDB; AB073662.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

PT useful as molecular targets for diagnosis, prophylaxis and treatment of

PS pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 5837; 455bp; English.

The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnosis,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biophysics technology. Sequences ABD01397-
 CC ABD01967 represent P. aeruginosa polynucleotides of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX Sequence 270 BP; 39 A; 92 C; 85 G; 54 T; 0 U; 0 Other;

Query Match 20.4%; Score 207.2; DB 11; Length 270;
 Best Local Similarity 85.8%; Pred. No. 7.2e-27;
 Matches 230; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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321  TACTTTTGAACCTGTTGAAAGAACCGACAGCCGATGCTGTCGCTGATCATCG 380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270  CTACTCTCTGACCTGTCGTCAGACACCGAAGAGCTTCTGTGTGCTGCTCATGCG 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
391  CCGCGGACCGGCAATGTCGCGGCAACGCGATGCTCAACCTGTACACGCGGTGGCGGCGC 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
210  CCGGCGACCGGCAATGTCGCGGCAACGCGATGCTCAACCTGTACACGCGGTGGCGGCGC 151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
441  CAGCAACAGACTGCGCGGCAAGGCGTGTGTGATGACATGAACAGAGATCAAGTC 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 150 CCGCGCAAGTCCGCGACGCGCGCAAGGCGCTGATCACCATTGAACGACGAGATCTCTTC 91
 QY 501 CCGCGCTGACCTGAGCAAGTGCATCAATCAAGACCGAAGCTTGAAGAGCGCCCTGGGG 560
 DB 90 CCGCGCGCGACGCGAGCAAGATGCTCAACATCAAGACCGAAGCGCTTCAAGAGCGCGGG 31
 QY 561 CCGCGCTGAGCATGCTGCTGGAAGCAAG 588
 DB 30 CCGCGTGGGCAATGCTGTGAGGCGAAG 3

RESULT 15

ADO07178
 ID ADO07178 standard; cDNA, 1303 BP.

XX ADO07178;

XX 15-JUL-2004 (first entry)

XX Aspergillus oryzae asparaginase coding sequence.

XX Asparaginase; enzyme; acrylamide; heat treatment; gene; ss.

XX Aspergillus oryzae.

XX Key Location/Qualifiers

XX FT CDS 49..1185

XX FT /tag a

XX FT /product "Asparaginase"

XX FT /EC_number "3.5.1.1"

XX MO2004032648-A1.

XX 22-APR-2004.

XX 10-OCT-2003; 2003WO-DK000684.

XX 11-OCT-2002; 2002DK-00001547.

XX (NOVO) NOVOZYMES AS.

XX Budolfesen G, Jensen MT, Heide-Hansen HP, Stringer MA, Lange L;

XX P-PSDB; ADO07179.

XX Preparing heat-treated product such as potato chips by providing raw

XX material having carbohydrate, protein and water, treating raw material

XX with enzyme reacting on asparagine or glutamine and heat treating to

XX reduce water content.

XX Claim 11; SEQ ID NO 1; 46bp; English.

XX The present sequence is that of cDNA encoding Aspergillus oryzae
 CC asparaginase. The cDNA was isolated from a cDNA library on the basis of
 CC homology to Saccharomyces cerevisiae asparaginase II. The enzyme shows
 CC optimal activity at pH 7 (at 37 degrees C) and 60 degrees C (pH 7.0) and
 CC is stable in the pH range from about 4.0 to 8.0. It has a molecular
 CC weight of 40-65 kDa (SDS-PAGE). A claimed method of reducing the
 CC formation of acrylamide during heat treatment of raw material comprising
 CC carbohydrate, protein and water involves treatment of the raw material
 CC with an enzyme prior to heat treatment. The enzyme may be an
 CC asparaginase, including A. oryzae asparaginase, that is capable of
 CC reacting on asparagine or glutamine (optionally substituted). The method
 CC is useful for preparing a heat-treated product (claimed) such as potato
 CC products, potato chips, breakfast cereals, biscuits, roasted nuts, hot
 CC cakes, pancakes, etc.

XX Sequence 1303 BP, 303 A; 421 C; 305 G; 274 T; 0 U; 0 Other;

XX Query Match 20.3%; Score 205.6; DB 12; Length 1303;

XX Best Local Similarity 56.5%; Pred. No. 1.3e-26;
 XX Matches 445; Conservative 0; Mismatches 334; Indels 9; Gaps 3;

QY 25 CTGGCAACGTGATGATCTTGGCAACCGCGGACCATGCGCGGCTGGCGCGAGCGG 84
 DB 199 CTGGCAACGTGATCTTGGCAACCGCGGACCATGCGCGGCTGGCGCGAGCGG 258
 QY 85 GCCAACAAGCGCACCTTACCAAGCTGCGCAAGATTGGCTGACAAAGTGAATTCGCGCTG 144
 DB 259 ACCGCAACAAGGTTTACAAAGCGGCTGCGATCGAGATCACTGATTCAGCGGCTG 318
 QY 145 CCGAGCTGGCGGACCTGGCGCAATGCGCGGCGAGAGTGAATGCAATGCCCTCCGA 204
 DB 319 CCGAATATCTAAAGTTCGCAACGCTGGCGGCTGCGAGTAACTGCGAGCGCA 378
 QY 205 AGCATCAACCAAGACGACCTGCTCAAGCTGGCAAGAGCGTGGCGGCGGCGCAAGC 264
 DB 379 GACATCACTTCCGCACTTCTCTGCTCTCTTCAACAGATCAACGAGTGGCTGCAAC 438
 QY 265 AA---TGAAGTCAATGCTGCTCAATCAACCAATGCAACCGAACCCTGGAGAAACCGGC 321
 DB 439 GACCCACATGCGCGGCTGCAATGCTGCAACCGAACCCTGGAGAAACCGGC 498
 QY 322 TACTTTGAACCTGCTGGAAGAAAGCAAGCGGATGCTGCTGCTGCTGCTGCTGCTG 381
 DB 499 TCTTCTTCAAGCGCAAGCTGCTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 558
 QY 382 CCGGCAACGCGCATGCTGCGCGCAAGCGCAAGCTGCTCAAGCGGCTGCTGCTGCTGCTG 441
 DB 559 CTTCAACCGCATGCTGCGCGCAAGCGCAAGCTGCTCAAGCGGCTGCTGCTGCTGCTG 618
 QY 442 AGCAACAAGAGTCTGCGCGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501
 DB 619 GCGAGCGCGCAAGCGGCTGCGCGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
 QY 502 GCGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 558
 DB 679 GCGTCTGAGCTGCAAGCGGCTGCAAGCGGCTGCAAGCGGCTGCAAGCGGCTGCAAG 738
 QY 559 GCGCGCGGCGGCTGCTGCGCGCAAGCGGCTGCTGCGCGGCTGCTGCGCGGCTGCTG 618
 DB 739 GGTAACTGCGGCGGCTGCTGCGCGCAAGCGGCTGCTGCGCGGCTGCTGCGCGGCTG 795
 QY 619 CACACGTCACCTCGAGTTCGACATCAAGCATGACGAGCTGCGCGGCTGCGGCTGCAATC 678
 DB 796 CCAACGCGCAAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 855
 QY 679 GCGTCAAGTATGCGCAAGCTCAACGCAAGCGGCTGCAAGCGGCTGCAAGCGGCTG 738
 DB 856 CTCTACTCATGCAAGAGCATGCAATGCAACCTTACTCGCGCATGCAACGCGCGCA 915
 QY 739 AAGCGCTGATCAATGCGCGCAAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 798
 DB 916 AAGGCGATGTTATGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 975
 QY 799 CTGACAGA 806
 DB 976 ATGGAAGA 983

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 Job time : 664 secs

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OW nucleic - nucleic search, using sw model

Run on: March 22, 2005, 07:01:33 ; Search time 216 Seconds
(without alignments)
7681.410 Million cell updates/sec

Title: US-09-842-628-1

Perfect score: 1014
Sequence: 1 aaggaagcgcgcgaaccagca.....ttctctggaactatcgataa 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	100.0	1014	5	PCT-US92-10421-1
2	983.4	97.0	1017	3	US-08-050-482A-1
3	742	73.2	1182	4	US-09-252-991A-5793
4	742	73.2	1135	4	US-09-252-991A-5877
5	562.2	55.4	2748	4	US-09-252-991A-5773
6	273	26.9	1125	4	US-09-328-352-2336
7	240.8	23.7	1848	1	US-08-447-422-15
8	240.4	23.7	1071	1	US-09-489-039A-730
9	219	21.6	1133	3	US-09-094-435-3
10	207.2	20.4	270	4	US-09-252-991A-5837
11	138	13.6	1830121	4	US-09-557-884-1
12	138	13.6	1830121	4	US-09-643-990A-1
13	129	12.7	1041	4	US-09-543-681A-1219
14	83	8.2	4403765	3	US-09-103-840A-2
15	83	8.2	4411529	3	US-09-103-840A-1
16	78.8	7.8	2772	4	US-09-252-991A-5838
17	72.2	7.1	963	4	US-09-583-110-925
18	72.2	7.1	966	4	US-09-107-433-791
19	66.8	6.6	1005	4	US-09-107-532A-1293
20	66.2	6.5	1002	4	US-09-134-000C-1208
21	65	6.4	1104	4	US-09-252-991A-9014
22	65	6.4	1425	4	US-09-252-991A-8780
23	65	6.4	1653	4	US-09-252-991A-10546
24	65	6.4	1701	4	US-09-252-991A-8997
25	64.6	6.4	1758	4	US-09-252-991A-8997
26	64.6	6.4	3120	4	US-09-902-540-6505
27	64.6	6.4	3122	4	US-09-902-540-469

28	64.4	6.4	1268	2	US-08-403-852D-2	Sequence 2, Appl1
29	64.4	6.4	1268	3	US-08-510-646B-2	Sequence 2, Appl1
30	64.4	6.4	1268	3	US-09-231-818-2	Sequence 2, Appl1
31	64.4	6.4	1268	4	US-09-635-359B-2	Sequence 2, Appl1
32	64.4	6.4	5392	2	US-08-403-852D-1	Sequence 1, Appl1
33	64.4	6.4	5392	3	US-08-510-646B-1	Sequence 1, Appl1
34	64.4	6.4	5392	3	US-09-231-818-1	Sequence 1, Appl1
35	64.4	6.4	5392	3	US-09-635-359B-1	Sequence 1, Appl1
36	64.2	6.3	876	4	US-09-252-991A-1565	Sequence 1565, Ap
37	64.2	6.3	1512	4	US-09-252-991A-1551	Sequence 1551, Ap
38	64.2	6.3	1677	4	US-09-252-991A-1616	Sequence 1616, Ap
39	62.8	6.2	2810	3	US-09-408-647A-1	Sequence 1, Appl1
40	62.4	6.2	1644	4	US-09-252-991A-792	Sequence 792, App
41	62.4	6.2	2907	4	US-09-252-991A-831	Sequence 831, App
42	62.4	6.2	49225	4	US-09-902-540-1269	Sequence 1269, Ap
43	61.8	6.1	1989	4	US-09-252-991A-15371	Sequence 15371, A
44	61.8	6.1	2058	4	US-09-252-991A-15462	Sequence 15462, A
45	61.8	6.1	2231	3	US-08-961-527-265	Sequence 265, App

ALIGNMENTS

RESULT 1
PCT-US92-10421-1
Sequence 1, Application PC/TUS9210421
GENERAL INFORMATION:
APPLICANT: Robert, Joseph
APPLICANT: MacAllister, Thomas W
APPLICANT: Sethuraman, Natrajan
APPLICANT: Freeman, Abbie G
TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND
TITLE OF INVENTION: ITS USE IN ANTIVIRAL AND ANTICANCER THERAPY
NUMBER OF INVENTIONS: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie and Beckett
STREET: 1001 G Street N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10421
CLASSIFICATION:
FILING DATE: 19921204
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P4140003.8
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00100.41200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PSEUDOMONAS 7A
PCT-US92-10421-1
Query Match 100.0%; Score 1014; DB 5; Length 1014;

Best Local Similarity 100.0%; Pred. No. 1e-209;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AAGGAAGTGAAGAACAGAGAGAGCTGGCAACGTGGTATCTGGGCAACGGCGGCAAC 60
DB 1 AAGGAAGTGAAGAACAGAGAGAGCTGGCAACGTGGTATCTGGGCAACGGCGGCAAC 60
QY 61 ATGCGCGGCGCTGGCGCCAGCGCGGCAACAGCGCCACTTACAGAGCTGGCAAGTTGCG 120
DB 61 ATGCGCGGCGCTGGCGCCAGCGCGGCAACAGCGCCACTTACAGAGCTGGCAAGTTGCG 120
QY 121 GTTCGACAGCTGATTTGGCGGCTGCGAGCTGGCGCACTTGGCCATATGCGCGCGAG 180
DB 121 GTTCGACAGCTGATTTGGCGGCTGCGAGCTGGCGCACTTGGCCATATGCGCGCGAG 180
QY 181 CAGGTGATGATGATGCTCCGAAAGCATCACCAACGACGACCTGCTCAAGCTGGCAAGC 240
DB 181 CAGGTGATGATGATGCTCCGAAAGCATCACCAACGACGACCTGCTCAAGCTGGCAAGC 240
QY 241 AGCGTGGCCGAGCTGGCGCCAGCAAGATGACGTGATGATGATGATGATGATGATGATG 300
DB 241 AGCGTGGCCGAGCTGGCGCCAGCAAGATGACGTGATGATGATGATGATGATGATGATG 300
QY 301 GACACCTCTGGAGAGAAACCGCTTACTTTTGAACCTCTGAGAAAGACCGACAGCGCATC 360
DB 301 GACACCTCTGGAGAGAAACCGCTTACTTTTGAACCTCTGAGAAAGACCGACAGCGCATC 360
QY 361 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 GCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 TACAAAGCGGTGGCGGTGGCGCAAGCAAGATGATGATGATGATGATGATGATGATGATG 480
DB 421 TACAAAGCGGTGGCGGTGGCGCAAGCAAGATGATGATGATGATGATGATGATGATGATG 480
QY 481 ATGAAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB 481 ATGAAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 541 GCGTTCAGAGAGCGCTGGGCGCGCTGGGCGATGATGATGATGATGATGATGATGATGATG 600
DB 541 GCGTTCAGAGAGCGCTGGGCGCGCTGGGCGATGATGATGATGATGATGATGATGATGATG 600
QY 601 CGCCTGCGCGCGCAAGCGCGCAACCGGTCACTCGAGTTGATGATGATGATGATGATGATG 660
DB 601 CGCCTGCGCGCGCAAGCGCGCAACCGGTCACTCGAGTTGATGATGATGATGATGATGATG 660
QY 661 CTGCGCCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 CTGCGCCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 CTGGGCAAGAGCGGCGCGCAAGCGCGCTGATGATGATGATGATGATGATGATGATGATG 780
DB 721 CTGGGCAAGAGCGGCGCGCAAGCGCGCTGATGATGATGATGATGATGATGATGATGATG 780
QY 781 TCGCGGAGTGTGCTGAGCGCTGAGAGAGCTGCGCAAGAGCGGCTGAGATGATGATGATG 840
DB 781 TCGCGGAGTGTGCTGAGCGCTGAGAGAGCTGCGCAAGAGCGGCTGAGATGATGATGATG 840
QY 841 TCAAGTCAAGAGGCGGCTTGTGCTGCTGAACGCTGAGAGAGCGCGCATCTGGCATGATG 900
DB 841 TCAAGTCAAGAGGCGGCTTGTGCTGCTGAACGCTGAGAGAGCGCGCATCTGGCATGATG 900
QY 901 TGGGTGCTGGCGCGCAAGCTGGAACCGCGAGAGGCGCGCATCTGGCATGATGATGATG 960
DB 901 TGGGTGCTGGCGCGCAAGCTGGAACCGCGAGAGGCGCGCATCTGGCATGATGATGATG 960
QY 961 ACCAAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
DB 961 ACCAAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014

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RESULT 2

US-08-050-482A-1
Sequence 1, Application US/08050482A
Patent No. 6312939

GENERAL INFORMATION:
APPLICANT: ROBERTS, Joseph
MACALLISTER, Thomas W.
SETHURAMAN, Natarajan

TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN ANTIVIRAL AND ANTICANCER THERAPY

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,482A
FILING DATE: 25-Apr-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US92/10421
FILING DATE: 04-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 023032/0106

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nucleic acid
STRANDNESS: double

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1011

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-050-482A-1

Query Match 97.0%; Score 983.4; DB 3; Length 1017;
Best Local Similarity 96.6%; Pred. No. 4.1e-203;
Matches 1003; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

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QY 1 AAGGAAGTGAAGAACAGAGAGAGCTGGCAACGTGGTATCTGGGCAACGGCGGCAAC 60
DB 1 AAGGAAGTGAAGAACAGAGAGAGCTGGCAACGTGGTATCTGGGCAACGGCGGCAAC 60
QY 61 ATGCGCGGCGCTGGCGCCAGCGCGGCAACAGCGCCACTTACAGAGCTGGCAAGTTGCG 120
DB 61 ATGCGCGGCGCTGGCGCCAGCGCGGCAACAGCGCCACTTACAGAGCTGGCAAGTTGCG 120
QY 121 GTTCGACAGCTGATTTGGCGGCTGCGAGCTGGCGCACTTGGCCATATGCGCGCGAG 180
DB 121 GTTCGACAGCTGATTTGGCGGCTGCGAGCTGGCGCACTTGGCCATATGCGCGCGAG 180
QY 181 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB 181 CAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 241 AGCGTGGCCGAGCTGGCGCCAGCAAGATGACGTGATGATGATGATGATGATGATGATGATG 300
DB 241 AGCGTGGCCGAGCTGGCGCCAGCAAGATGACGTGATGATGATGATGATGATGATGATGATG 300

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QY 301 GACACCTGGAAAGAAACGGCTACTTTTGAACCTGTGAAAGAAAGACGACGACCGATC 360
DB 301 GACACCTGGAAAGAAACGGCTACTTTTGAACCTGTGAAAGAAAGACGACGACCGATC 360
QY 361 GTGCTGTGTGCTTCCATGAGCGCCCGACCGCCATGTCGCGGACGCGCATGCTCACTG 420
DB 361 GTGCTGTGTGCTTCCATGAGCGCCCGACCGCCATGTCGCGGACGCGCATGCTCACTG 420
QY 421 TACAAAGCGCTGAGCGCTGAGCAAGAACTGCGCGGCAAGGCGCTGCTGTGACC 480
DB 421 TACAAAGCGCTGAGCGCTGAGCAAGAACTGCGCGGCAAGGCGCTGCTGTGACC 480
QY 481 ATGAAAGAGAGATCCAGTCCCGGCGTGAAGTGAAGATCCAACTCAAGACCGAA 540
DB 481 ATGAAAGAGAGATCCAGTCCCGGCGTGAAGTGAAGATCCAACTCAAGACCGAA 540
QY 541 GCCTTCAAGAGCGCTGAGCGCGCTGAGCAATGCTGAAAGCAAGTCTGACTGTTT 600
DB 541 GCCTTCAAGAGCGCTGAGCGCGCTGAGCAATGCTGAAAGCAAGTCTGACTGTTT 600
QY 601 CGCTTCCAGAGCGCGCCACAGGCTCACTCCGAGTTGCACTCAAGAGATCAGACAC 660
DB 601 CGCTTCCAGAGCGCGCCACAGGCTCACTCCGAGTTGCACTCAAGAGATCAGACAC 660
QY 661 CTGCCCCAGAGTGAATGCGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
DB 661 CTGCCCCAGAGTGAATGCGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
QY 721 CTGCGACAGAGCGCGCCAGAGGCTGATCAATGCGCGACCGGCAATGCTGCTGTG 780
DB 721 CTGCGACAGAGCGCGCCAGAGGCTGATCAATGCGCGACCGGCAATGCTGCTGTG 780
QY 781 TCGCGGTGTGTGCGAGCGCTGCGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TCGCGGTGTGTGCGAGCGCTGCGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 TCAC---GTCAAGAGCGGCTTCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 897
DB 841 TCAC---GTCAAGAGCGGCTTCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 897
QY 898 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 957
DB 898 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 957
QY 901 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 960
DB 901 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 960
QY 958 ATGACCAAGACCCAG 1014
DB 958 ATGACCAAGACCCAG 1014

RESULT 3

US-09-252-991A-5793
Sequence 5793, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5793
LENGTH: 1182
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5793

Query Match 73.2%, Score 742, DB 4, Length 1182;

Best Local Similarity 83.9%; Pred. No. 5,3e-151;
Matches 851; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 AAGAAAGTGAAGAACACGACGAGAGCTGAGCAACGTGTGATCTCTGACCGCGCGACCC 60
DB 1 AAGAAAGTGAAGAACACGACGAGAGCTGAGCAACGTGTGATCTCTGACCGCGCGACCC 228
QY 61 ATGCGCGGCGCTGAGCG 120
DB 61 ATGCGCGGCG 288
QY 121 GTGCAAGAGCTGATTTGCG 180
DB 121 GTGCAAGAGCTGATTTGCG 348
QY 181 CAGGTGATGACAGATGCTTCCGAAAGCATCAACCAAGACCTGTCAAGCTGTGACAGC 240
DB 181 CAGGTGATGACAGATGCTTCCGAAAGCATCAACCAAGACCTGTGTGAGAGCTGTGAG 408
QY 241 AGCGTGGCGGAGCTGGCG 300
DB 241 AGCGTGGCGGAGCTGGCG 468
QY 301 GACACCTGGAAAGAAACGGCTACTTTTGAACCTGTGAAAGAAAGACGACGACCGATC 360
DB 301 GACACCTGGAAAGAAACGGCTACTTTTGAACCTGTGAAAGAAAGACGACGACCGATC 528
QY 361 GTGCTGTGTGCTTCCATGAGCGCCCGACCGCCATGTCGCGGACGCGCATGCTCACTG 420
DB 361 GTGCTGTGTGCTTCCATGAGCGCCCGACCGCCATGTCGCGGACGCGCATGCTCACTG 588
QY 421 TACAAAGCGCTGAGCGCTGAGCAAGAACTGCGCGGCAAGGCGCTGCTGTGACC 480
DB 421 TACAAAGCGCTGAGCGCTGAGCAAGAACTGCGCGGCAAGGCGCTGCTGTGACC 648
QY 481 ATGAAAGAGAGATCCAGTCCCGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 540
DB 481 ATGAAAGAGAGATCCAGTCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 708
QY 541 GCCTTCAAGAGCGCGCTTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
DB 541 GCCTTCAAGAGCGCGCTTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 768
QY 601 CGCTTCCAGAGCGCGCCACAGGCTCACTCCGAGTTGCACTCAAGAGATCAGACAC 660
DB 601 CGCTTCCAGAGCGCGCCACAGGCTCACTCCGAGTTGCACTCAAGAGATCAGACAC 828
QY 661 CTGCCCCAGAGTGAATGCGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720
DB 661 CTGCCCCAGAGTGAATGCGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 888
QY 721 CTGCGACAGAGCGCGCCAGAGGCTGATCAATGCGCGACCGGCAATGCTGCTGTG 780
DB 721 CTGCGACAGAGCGCGCCAGAGGCTGATCAATGCGCGACCGGCAATGCTGCTGTG 948
QY 781 TCGCGGTGTGTGCGAGCGCTGCGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 781 TCGCGGTGTGTGCGAGCGCTGCGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1008
QY 841 TCAC---GTCAAGAGCGGCTTCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 900
DB 841 TCAC---GTCAAGAGCGGCTTCTGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1068
QY 898 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 957
DB 898 GACTGGGTGTGTGCGCGACGACCTGAACCGCGAGAGAGCGCGCATCTGTGCGATGTGGA 1128
QY 958 ATGACCAAGACCCAG 1011
DB 958 ATGACCAAGACCCAG 1182

RESULT 4

US-09-252-991A-5877/c
 ; Sequence 5877, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 5877
 ; LENGTH: 1335
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-5877

Query Match 73.2%; Score 742; DB 4; Length 1335;
 Best Local Similarity 83.9%; Pred. No. 5,4e-151;

Matches 851; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

QY 1 AAGGAAGTGAAGACGAGCAAGCTGCGCAAGTGTGATCTGCGCAACCGCGCGCAC 60
 DB 1239 AAGGAAGTGAAGACGAGCAAGCTGCGCAAGTGTGATCTGCGCAACCGCGCGCAC 1180
 QY 61 ATGCGCGGCGCTGGCG 120
 DB 1179 ATGCGCGGCG 1120
 QY 121 GTGCGCAAGCTGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 DB 1119 GTGCGCAAGCTGATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1060
 QY 181 CAGGTGATGCAATGCTCTCGAAGCATCACCAAGCATCTGCTCAAGCTGCGCAAGC 240
 DB 1059 CAGGTGATGCAATGCTCTCGAAGCATCACCAAGCATCTGCTGAGAACCTGCGCAAG 1000
 QY 241 ACGGTGCGCGAGCTGCG 300
 DB 999 ACGGTGCGCGAGCTGCG 940
 QY 301 GACACCTGGAAGAAACCGCTACTTTTGAACCTGTGAAAGACCGACAGCGGATC 360
 DB 939 GACACCTGGAAGAAACCGCTACTTTTGAACCTGTGAAAGACCGACAGCGGATC 880
 QY 361 GTGCTGTGCTGATTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 DB 879 GTGCTGTGCTGATTCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 820
 QY 421 TACCAAGCGGTGCG 480
 DB 819 TACCAAGCGGTGCG 760
 QY 481 ATGAACGAGAGATTCAGTCCCGGCGGTGAGAGCAATGATCAATCAAGACCGAA 540
 DB 759 ATGAACGAGAGATTCAGTCCCGGCGGTGAGAGCAATGATCAATCAAGACCGAA 700
 QY 541 GCGTTCAAGAGCGCTGCG 600
 DB 699 GCGTTCAAGAGCGCTGCG 640
 QY 601 CGCGTGCAGCG 660
 DB 639 CGCGTGCAGCG 580
 QY 661 CTGCGCGCGAGTGAATGCTTACAGCTATGAGCAAGTCAACGCGCGCGCGCGCGCGCG 720
 DB 579 CTGCGCGCGAGTGAATGCTTACAGCTATGAGCAAGTCAACGCGCGCGCGCGCGCGCG 520

QY 721 CTGCGCAAGAACG 780
 DB 519 CTGCG 460
 QY 781 TCGCGCGGTGCG 840
 DB 459 GCGCGCGGTGCG 400
 QY 841 TCAC---GTCAACAGCG 897
 DB 399 TCGCAAGTCAATGCG 340
 QY 898 GACTGGTGTGCG 957
 DB 339 GACTGGTGTGCG 280
 QY 958 ATGACCAAGACCGCGAGAGAGAGTGAAGCGCATTTCTGGAATGTA 1011
 DB 279 ATGACCAAGACCGCGAGAGAGTGAAGCGCATTTCTGGAATGTA 226

RESULT 5

US-09-252-991A-5773
 ; Sequence 5773, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 5773

; LENGTH: 2748

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

Query Match 55.4%; Score 562.2; DB 4; Length 2748;
 Best Local Similarity 85.2%; Pred. No. 4e-112;
 Matches 640; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

QY 264 CAATGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
 DB 1 GATGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 324 CTTTGAACCTGCGGAAAGACCGAAGACCGATCGTGTGCGTTCCATGCGCC 383
 DB 61 CTTTGAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 384 CGGCGCGCGATGTCG 443
 DB 121 GGGCGCGCGATGTCG 180
 QY 444 CAACAGAGATTCG 503
 DB 181 GACCAAGTCG 240
 QY 504 GCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 563
 DB 241 CGGCGCGCGAG 300
 QY 564 GCTGGGCGAGTGTGGAAGCAAGTCTACTGTTCCGCGCGCGCGCGCGCGCGCGCGCG 623
 DB 301 GCTGGGCGAGTGTGGAAGCAAGTCTACTGTTCCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 624 GGTCACTTCGAGTTCATCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCAATCA 683

Db 361 GGTGAATCTCCGAGTTTCAGATCAAGAGATCTCCGCGTGGCTCCGGTGAATAATCGCTTA 420
 QY 684 CAGCTATGGCAAGTCAACGCAACGCGCTTAACAAAGCCCTGGCAAGAAAGGCGCAAGGC 743
 Db 421 CAGCTACGGCAAGTCAAGCAACGCGCTTAACAAAGCCCTGGCAAGAAAGGCGCAAGGC 480
 QY 744 GCTGATTCATGCGCGCAACGCGCAATGCTCGGTGTCGTGCGGTGTCGTGCGGTGTCGTGCA 803
 Db 481 GATCATTCATGCGCGCAACGCGCAATGCTCGGTGTCGTGCGGTGTCGTGCGGTGTCGTGCA 540
 QY 804 GAGCTGCGCAAGAAAGCGGTGCAATCATTTGCTGCTAC--GTCAACAGGCGGCTTT 860
 Db 541 GGAATGCGCGCAAGGCGGTGCAATCATTTGCTGCTAC--GTCAACAGGCGGCTTT 600
 QY 861 CGTGTGCGCTTAACGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCT 920
 Db 601 CGTGTGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCT 660
 QY 921 GAACCGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 980
 Db 661 GAACCGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 720
 QY 981 GAGCTGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 1011
 Db 721 GAGCTGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 751

RESULT 6

US-09-328-352-2336
 ; Sequence 2336, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 2336
 ; LENGTH: 1125
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-2336

Query Match 26.9%, Score 273, DB 4, Length 1125,
 Best Local Similarity 56.2%, Pred. No. 8, 4e-50,
 Matches 557, Conservative 0, Mismatches 425, Indels 9, Gaps 2;

QY 30 CAGCGTGGATCTGCGCAACGCGCGCAATCGCGCGCGTGGCGCGCAAGCGCGCGCA 89
 Db 135 CAGTGTGTTGTTGCTGCTACTGCGCGTACATGCTGCTGCGCGCAAGCTCAGCAAA 194
 QY 90 CAGCGCACTTACAGGCTGCGCAAGTGGCGTCAAGCTGATTCGCGCGTGGCGCGCA 149
 Db 195 TAGTGAATCTTAAGCGCGCAAGTTCAGTGAATGCTTAATGAATGAGTTCCTCA 254
 QY 150 GCTGCGCACTGCGCAATGTCGCGCGCAAGAGTGAATGCAATGCTTCGGAAGCAT 209
 Db 255 AATTCAGATTTGCGCAATGATCTGCTATTCAGATTAAGATGCTTCGAAGATAT 314
 QY 210 CAGCAAGCGACGCTGCTCAAGTGGCAAGCGCGCGCGTGGCGCGCAAGCAATATA 269
 Db 315 TACTGCAAGGAAATTAACAAATGCTGCTCAAGTAATGAATCTTTAAAAAGCAAC 374
 QY 270 CCGTCAATGCGATGTCATCAACCATGCGCAACCTCGAAGAAAGCGCGCTACTTTT 329
 Db 375 TGTAAATGCGTGTGATTAACAACGCTACAGATCTTTAAGAAAGCAAGATTTTCTT 434
 QY 330 GAACCTGCGTGAAGAACCGCAAGCGCATGCTGCTGCTGCTTCATGCGCGCGCAC 389
 Db 435 AATCTGTGTTGCTACTGATTAACCAATGCTACTGTTGCTCAATGCGCGCATCAAC 494

QY 390 CCGCATGTCGCGCGCAAGCGCATGCTCAACCTGTACAAAGCGCGTGGCGCGCAAGCAAA 449
 Db 495 TCGCTTTTCAAGATATGTCATTAACCTTTATATGCTGTGATTTGGCGGCTTCTGA 554
 QY 450 GGAATCGCGCGCAAGGCGTGTGTCATGAAAGCAAGATCAATCGCGCGCTGA 509
 Db 555 TGAATCAAAATAAAGGCGTATGCTTCTCATGAACGACTGATTTTGTGCTGCTGA 614
 QY 510 CGTGAAGCAATGATCAATCAAGCAAGCGAAGCTTCAGAAAGCGCGTGGCGCGCGTGG 569
 Db 615 TGTAACTAAAGCATTAATTCATTAATCAATGCTTTTGAACCAATGCGGTGCTTTGG 674
 QY 570 CATGTGTGTAAGGCAAGCTGCTACTGCTTCCGCTGCGCGCAAGCGCGCAAGCTGA 629
 Db 675 TACATGTTGTAAGCAACATATTTGTTAGCAATGTTTAAAGCTATACCAATGCG 734
 QY 630 CTCGAGTTGACATCAAGCAATGACAGC-----CTGCCCAAGTGAACATGCGCTTA 683
 Db 735 TTCAAGATTTAATTAAGAAATATTAAGGTGATGCTTCCGACAGTCAAAATGCTTTA 794
 QY 684 CAGCTATGCGCAAGTCAACGCGCAACGCGCTCAAGAGCGCTGCGCAAGAAAGCGCGCAAGGC 743
 Db 795 TGGTCTGACTGCTATGCTTCTGATGCTTATGAGCATATGCAAAAGCTGCGCTTAAAGC 854
 QY 744 GCTGATTCATGCGCGCAACGCGCAATGCTCGGTGTCGTGCGCGGTGTCAGACCTTGA 803
 Db 855 GATTAATTCATGCAAGGTAAGGTAATGTTCTGTAGCAAAATATTCGTTTCAACATTA 914
 QY 804 GAGCTGC--GCAAGAAAGCGGTGCAATCATTTGCTGCTCAAGCTCAAGGCGGTTT 860
 Db 915 AATCTTCAATGCAAAAGCGGTATCAATTAATTCGCTCATGCGCGGTTTCAAGGTTT 974
 QY 861 CGTGTGCTTAACGCGCGCAAGCGCGCAACGCGCAAGAAAGCAAGTGGTGTGCGCGCAACCT 920
 Db 975 TGTATTAAGTGAATGCAAGCAAGCTGATCTTAATATGTTGGTGAAGCTCATGATTT 1034
 QY 921 GAACCGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 980
 Db 1035 GAATCTCAAAAGGCGGCTTCTTGGCGCGTGGCACTTACCAAAACCAAGATGCGAA 1094
 QY 981 GAGCTGCGCAAGGCGCGCATCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 1011
 Db 1095 AGAAATTCAGCAAGCTGCTGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCA 1125

RESULT 7

US-08-447-422-15
 ; Sequence 15, Application US/08447422
 ; Patent No. 5686579
 ; GENERAL INFORMATION:
 ; APPLICANT: SHAMT, Ezekiel Y.
 ; APPLICANT: ROTHSTEIN, Aber
 ; APPLICANT: RAMJESINGH, Mohabir
 ; TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
 ; TITLE OF INVENTION: Protect or Modulate Biological Activity
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/447,422
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/081,410

FILING DATE: 22-JUN-1993
 APPLICATION NUMBER: US 07/938,505
 FILING DATE: 31-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/205,748
 FILING DATE: 21-JUN-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 17923/102 HYL
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1848 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-447-422-15

Query Match 23.7%; Score 240.8; DB 1; Length 1848;
 Best Local Similarity 55.0%; Pred. No. 8,4e-43;
 Matches 542; Conservative 0; Mismatches 432; Indels 12; Gaps 3;

29 CCAACGTGGTGAATCTCTGGCCACCGGCGGACCATCGCGCGCTGAGCGCCAGCGGCGCA 88
 872 CCAATATCAACCAATTTAGCAACCGCGGACCATTTGCGGTGTGTACTCCGACCA 931
 89 ACAGCGCCACCTTACCAAGCTGCGCAAGTTGGCTGACAGTGAATGGCGGCGCGG 148
 932 A---ATCTAATCAACAGTGGGTTAAAGTTGGCTGAAATCTGTTAATGCGGTGCGCG 988
 149 AGCTGGCGGACCTGGCCATATGCGCGGAGACAGGTATGAGATTCGCTCCGAAGA 208
 989 AACTAAAGACATGTGGAGCGTTAAAGGAGACAGGTAGTAATTCGCTCCAGACA 1048
 209 TCACCAACGACGACCTGTCTCAAGCTGGCAAGCGGTGGCCGAGCTGGCCGACGAATG 268
 1049 TGAAGATTAATGTCTGGCTGACACTGGCGAATAAATTAC-----ACCGATCGGAT 1102
 269 ACGTGGATGCAATCGTCATCACTGACCCATGGCAACCGACCTCTGAGAAACCGCTTACTTT 328
 1103 AGACCGACGCGCTTCGTCAATTAACCGTACCGACACGATGAGAAACCTGCTTACTTCC 1162
 329 TGAACCTCGTGAAGAAAGACCGACAGCGATGCTGCTGCTTCATGCGGCCCGCGCA 388
 1163 TCGACCTGACGGTGAAGATGCAACAAACCGGTGTGTATGCTGGCGCAATGCGTCTGCA 1222
 389 CGGCATGTCGCGCGACGCGCATGCTCAACCTGTACAAACCGCTGGCCGTCGACCAACA 448
 1223 CGTCTATGAGCGCAACGCTTCATTAACCTGTATACCGGTTATGACCGGACGCTGAT 1282
 449 AGAGCTCGGCGCGCAAGGCGTGTGTGTGACATGAAACGACGATTCAGTCCGAGCGTG 508
 1283 AAGCTCCGCGCAACGCTGGCGTGTGTGTGTATGATGAATGACACGCTGCTTGAATGCGCGTG 1342
 509 ACGTGAAGATGCTGATCAACATCAAGACCGAAGCTTTCAAGAGCG---CTTGGGGCGCGC 565
 1343 ACGTACCAAAACCAACACACCGACGTAAGCACTTCAAGTCTTAACTAAGGTCTCTC 1402
 566 TGGGATGGTGTGGAAGGACAGTGTGTTGCTGCGCTGCGGCGCAAGCGCCACAGCG 625
 1403 TGGGTACTTACCAACGTTAAGATTGATTAACAGGTATCCCGGCACTAGACATACA 1462
 626 TCACTCCGAGTTTCAATCAAGACGATGACAGCGCTGCGCAAGCTGATGACCTGCTACA 685
 1463 GCGACACGCGCATTCATGCTCTTAAGCTGAATGAATCGCGCAAGCTGCTTTTATA 1522
 686 GGTATGCGAAGCTCAACGACAGGCTTACAAAGGCTTGGCAAGAAAGCGGCGCAAGCGCGC 745
 1523 ACTACGCTAACGCGATCTTCCTTCCGGCTTAAAGCACTGGTATGCGGCTATGATGCA 1582

746 TGATTCATGCGCGGACCGGCAATGCTCGGTGCTGCGGGGTGTGTCAGCCTTCAGG 805
 1583 TCGTTAGCGGTGTGTGTGTGTAACGCAACCTGTATTAATCTGTGTGACACGCTGGCGGA 1642
 806 AGCTGCGCAAGACGGCGTGTGACATCTGCTTGTGTACCTTCACAGGCGGTTTCGTG 865
 1643 CCGCGCGCAAAACCGGTACTGCACTGCTGCTTCTTCCCGGTACCGACGCGCGCTACCA 1702
 866 TGGCTAACCGGACGACAGCCGACCAAGACACTGAGTGTGCGCCACGACTGAAC 925
 1703 CTCAGATGCGCGAAGTGTATATGCGAATACGGCTTGTGCTGCTTGGCACTGCAAC 1762
 926 CGCAAGAGCGCGCATCTGCGATGTGTGCAATGACCAAGACCCGACAGCAAGAGC 985
 1763 CGCAAAAGCGCGGCTTGTGCTGCAACTGCTGACGCAACCAAGATCCGACGACAGA 1822
 986 TGCAGCGCATTTTCTGGGAATCTGA 1011
 1823 TCCAGCAGATCTTCATCACTCACTAA 1848

RESULT 8
 US-09-489-039A-730
 Sequence 730, Application US/09489039A
 Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709,2004001
 CURRENT FILING DATE: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 730
 LENGTH: 1071
 TYPE: DNA
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-730

Query Match 23.7%; Score 240.4; DB 4; Length 1071;
 Best Local Similarity 54.2%; Pred. No. 9.1e-43;
 Matches 543; Conservative 0; Mismatches 441; Indels 18; Gaps 2;

13 AACACGAGAAAGCTGGGCAAGGTGTATCTGGGCAACGGGCGGACCATGCGCGGCT 72
 85 AGCGAGACGCGCTTCCGATATTTGTTATTTTACCAACGGCGGACGATTTGCTGTTG 144
 73 GCGCGACGCGGCGCAACGCGCACTTACAGGCTGCAAGTTGGCTGACAAAGCTG 132
 145 GCGGCGACATATCCAAACAAACCGGCTATAAGCGCGGAGTATGGGTGCAAGCGCTG 204
 133 ATTGCGGCGTGGCGGAGCTGCGGACCTGCGCAATGTGCGCGGTGAGAGATGACG 192
 205 ATTAAAGCGCGTGGCGGAATGATTAATCTCTACGTCGAGGGGAGACAGTGGCCAT 264
 193 ATGCGCTCCGAAAGATACCAAGACGACGACCTGCTCAAGCTGGCAAGAGCGGTGCGAG 252
 265 ATTGCGATGGAATATGACAGCGATATTAATCTTCAGCTCTCGAAGCGGTGATGATG 324
 253 CTGGCGGACAGCAATGACGATGATGATGCTATCAACCTTACAGGACCGACCACTGANA 312
 325 CTATTGGCTGGGAGGATGTGATGCGGTGTGATCAACCAATGGACGAGACACGCTGAT 384
 313 GAAACCGCTTACTTTTGAACCTGTGTGAAAGACGACAGCGGATGCTGTGTGCT 372
 385 GAAACCCCGTATTTCTCAATCTGACGCTGAAAGCAAGAGCGGTGTCTTTTACCGCG 444
 373 TCCATGCGCGCGGAGACGCGATGCTGCGGACGCGCATGCTCAACCTGTAAACGCGGTG 432
 445 GCGATGCGCGCGGAGACGCGATGACGCGGACCGGCGGATGATCTGCTGGAAGCGGTG 504

433 GCGTGGCCAGCAAGAGGATCGCGCGGCAAGGCGTGTGATCATGACGACGAG 492
 505 AGCGTGGCGCGGATCTCTATGCTCCGGGAGACCGCGGATATGCTGCTTAACGACCGC 564
 493 ATCCAGTCCGGCGGTGACGTGACGATGATCAATCAAGACCGACCTTCAAGAC 552
 565 ATCGGCGCGCGGCTTGTGACCAAAATCAATGCACTTGGTGAATACCTTCCGGGG 624
 553 GCGTGGG--GCGCGTGGGCAATGCTGTGAAAGGAAATGATGATCTGCTTCCGCTGCG 609
 625 CCGGAGAGGCGTATCTTGTGTGTGCTGTGCGGCGGAAAAAGCCAGTTCAGACGCGGGTG 684
 610 GCCAGCGCGCACAGGCTCAACTCCGAGTTGCAATCAAGCAATGACGACCTGCGCCGAG 669
 685 GATTAATTTACACGCTGCGCTGCGTGTGATGCTGATGCTGAGAGTTCTGCGCGAAG 744
 670 GTGACATGCTGCTTACGATGATGACGATGACGACGCGCTTACAAAGCGCTGCGACAG 729
 745 GTGGATATTATTTATGTTATACAGAGACGATCCGAGATATATGATGATGCGGAGATCGCC 804
 730 AACGCGCCAGGCGCTGATTCATGCTCGGACCGGCAATGCTGCTGTGCGCGGGTG 789
 805 CATCATGCGGAGGTATATCTATACGCGGACCGGCGGCGGTGCTGTGCTGCTAGT 864
 790 GTGCGAGCGCTGACAGGAGCTGCGCAAGAACGGGCTGACATCATCTGCTGTGCTGCA 849
 865 GCGCGCGGTATCAAAAGAGCGACGAGCGGCGATGCTGTGTGAGAGCTTCCGCTAC 924
 850 CAGGCGGTTTGTGTGCTGCTGATACGCGGACGAGCCCGACGACAAAGAACGCTGCTG 909
 925 GCGAGCGGCGGTGATCCGCGGATGACGACGCGCG-----GTTGTG 969
 910 GCGCAGACCTGTAACCGCGAAGGCGCGCATCTGCGCATGTGCGCATGACCAAGACC 969
 970 GCGGACTCCCTCAACCGCGCAAGGCGCGTATCTGCTGATGACGCGCTGACGCGACT 1029
 970 CAGGACAGAGAGCTGACGCGCATTTTCTGGAATACTGA 1011
 1030 AAGATCCGACGATTCAGCAATTTTCATCTACTCTGA 1071

RESULT 9 US-09-094-435-3

Sequence 3, Application US/0904435

Patent No. 6251388

GENERAL INFORMATION:

APPLICANT: Donald L. Durden

TITLE OF INVENTION: UTILIZATION OF MOLINELLA SUCCINOGENES

TITLE OF INVENTION: ASPARAGINASE IN THE TREATMENT OF HUMAN

TITLE OF INVENTION: HEMATOLOGIC AND AUTOIMMUNE DISEASE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,435

FILING DATE: Filed Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/049,085

FILING DATE: June 9, 1997

APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weidberg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 234/274
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELETYPE: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1133 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-094-435-3

Query Match 21.6%; Score 219; DB 3; Length 1133;
 Best Local Similarity 52.8%; Pred. No. 3.8e-38;
 Matches 521; Conservative 0; Mismatches 460; Indels 6; Gaps 2;

29 CCAAGTGTGATCTTGTGCGACCGGCGGACCATGCGCGCTGCGCGGCGGCGGCA 88
 128 CCAAGTGTGATCTTGTGCGACCGGCGGACCATGCGCGCTGCGCGGCGGCGGCA 187
 89 ACAAGCGCACCTTACCAAGCTGCGGAGTGGCTGCAAGGATGATGCGCGGCTGCGG 148
 188 AGAG---TAGTACTCTGTGTGAGAGATGACCGTTGATTAAGCTTGTGAGCGCTG 244
 149 AGCTGGCGACCTTGTGCGGACATGCGCGGCGGAGCATGATGATGCGCTTCCGAAGA 208
 245 CCATCAAGACCTTACCAAGCTGCGGAGGATGATGATGATGATGATGATGATGATGAT 304
 209 TCACCAAGACGACCTTGTGCGGAGGATGATGATGATGATGATGATGATGATGATGAT 268
 305 TGACGGGTAAAGGTGTGCTTAAATAGCAAGCGGTGCAATGAGCTCTGCGCAAAAG 364
 269 AGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 328
 365 AGACCGAAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424
 329 TGAACCTGTGTGAAAGACCGGACGAGCGGATGCTGTGCTGCTGCTGCTGCTGCTG 388
 425 TCAACCTGACGCTGAAAGACCGGACGAGCGGATGCTGTGCTGCTGCTGCTGCTGCT 484
 389 CCGCATGTGCGCGGACGAGCATGCTCAACCTGTCAACGCGGTGCGCGGTGCGGCAACA 448
 485 CTTCAATGATGCTGATGCGGCGGATGATGATGATGATGATGATGATGATGATGATGAT 544
 449 AGGATCTGCGCGGCAAGGCGGTGCTGTGATGATGATGATGATGATGATGATGATGAT 508
 545 AAGCTCTTACTTAAAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 604
 509 AGGTGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
 605 AAGCAACAGCTTCAACACCGGACGATGATGATGATGATGATGATGATGATGATGATGAT 664
 566 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 625
 665 TGGGACAGTGTATATGAGCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 724
 626 TCAACTCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 685
 725 TTGCAAGTGAAGTTATATGCAAAATGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 784
 686 GGTATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 745
 785 CTCACCGCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
 746 TGATCATGCGCGGACCGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 805
 845 TCATCATGCGCGGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATGCGCAATG 904

QY 806 AGCTGCGAAGACGGCGTGCAGATCATTCGTTGTCAGTCACAGAGGGCGTTTCGTC 865
 DB 905 AAGCAGCCAAATACAGCCGAGTCGTCTGCTGCAAGCTCTAGAGTGGGCGAGTTCACACA 964
 QY 866 TCGGTACGCGCGAGACCCGACGACAGACGACTGGGTGTCGCGCCACGACTGAACC 925
 DB 965 CCGAAGAGCTGATGATGATTAAGAACTTGTGCTACAGAGAGTCTCAACC 1024
 QY 926 CGCAGAGCCCGCATCTCGGCGATGTCGATGACCAAGACCCAGACAGAGAGGAC 985
 DB 1025 CTCAAAAAGCCAGAGTCTTCTTAATGTTAGCCCTCACAAAATGATGATAGAGAGCA 1084
 QY 986 TCGACGCGATTTCTGGAATACTGAT 1012
 DB 1085 TCCAAAAGATCTTCTCCACCTATTAAT 1111

RESULT 10
 US-09-252-991A-5837/c

; Sequence 5837, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 5837
 ; LENGTH: 270
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-5837

Query Match 20.4%; Score 207.2; DB 4; Length 270;
 Best Local Similarity 85.8%; Pred. No. 9.7e-36;
 Matches 230; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 321 CTACTTTTGAACCTCGTGAAGAAAGACGACAGCCGATCGTGTGCGTTCCATGCG 380
 DB 270 CTACTTTCGACCTCGTGTGACACACGAGAGCTTACGTGTGTGCGTTCATGCG 211
 QY 381 CCCCAGCAGCCGATGTCGCGACGCGATGCTCAACCTGTACAAAGCCGTCGTCG 440
 DB 210 CCGGAGCAGCGGATGTCGCGACGCGATGCTCAACCTGTACAAAGCCGTCGTCG 151
 QY 441 CAGCAACAGAGCTGCGCGGAGAGGCGTGTGTGACCAAGAAAGCAAGATCAAGTC 500
 DB 150 CGGCGACAGAGTGGGACGCGGAGAGGCGTGTGTGACCAAGAAAGCAAGATCTCTC 91
 QY 501 CGGCGGTGACGTGACAGTGCATCAACATCAAGACCGAGCTTCAAGAGCGCTGAGG 560
 DB 90 CGGCGCGACGCGAGCAAGATGTCAACATCAAGACCGAGGCTTCAAGAGCGCTGAGG 31
 QY 561 CCGGCTGGGATGTGTGTGAAGGCAAG 588
 DB 30 CCGGCTGGGATGTGTGTGAAGGCAAG 3

RESULT 11

US-09-557-884-1
 ; Sequence 1, Application US/09557884

; GENERAL INFORMATION:
 ; APPLICANT: Fleischmann et al.
 ; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,884

FILING DATE: 25-Apr-2000

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1

Query Match 13.6%; Score 138; DB 4; Length 1830121;
 Best Local Similarity 48.5%; Pred. No. 6.1e-20;
 Matches 474; Conservative 0; Mismatches 491; Indels 12; Gaps 3;

QY 40 ATCTGCGACCGCGGACACCATGCGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 99
 DB 802735 ATCTGCGACCGCGGACACCATGCGCGGCTGCGGCGGCGGCGGCGGCGGCGG 802791
 QY 100 TACAGGCTGCGCAAGTTGCGGTGACACAGTGTGCGGCGGCGGCGGCGGCGGCGG 159
 DB 802792 TATTAAGCTGACATTAAGTATGATCTTTAATTGAAGCTGTACCAAGAAATGA 802851
 QY 160 CTGGCAATGTGCGCGGCGGACAGGTGATGCAATGCGCTCCGAAGCATGACCAAGCAG 219
 DB 802852 ATTGCAACATTAAGGTGACCAATGTTAATAAGTTTCAACAAGATGATGACGAA 802911
 QY 220 GACTGTCTCAAGCTGCGCAAGAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 279
 DB 802912 GTCTGGCTTAAGCTGCGCAAGAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 802965
 QY 280 ATGCGATCACCAATGCGGACGACACCTGGAAGAAACCGCTTCTTTGAACCTCGTG 339
 DB 802966 TTGTGATTAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803025
 QY 340 GAAAAGCCGACAGCCGATGTCGTGTCGTTCCATGCGCGCGGACCGCCATGTC 399
 DB 803026 GTAAATGTGAAAACCGGTTGTTCTGTTGGGCAATGCGCTTCTGCAACGAAAAGT 803085
 QY 400 GCGGAGCGATGCTCAACCTGTGACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
 DB 803086 GCTGATGCGCATTAATCTTTAAGATGCTGTTGTGCGAGCAGCAAGAAAATCAAGT 803145
 QY 460 GCGAAGCGGCGGTGTCGATGACATGACAGAGATTCAGTCCGGGCGTGAAGTGAGCAG 519
 DB 803146 GGTGCTGTTTGAAGTGCATGATATATGATGATGATGATGATGATGATGATGATGAT 803205

Qy	520	TCGATCAACATGAGACCGAAGCCTTCAAGAGGC---CTGGGGGCCGTCGGGCATGGTG	576
Db	803206	ACCAATACGACCGCAGTCGAAACGTTCCATTCAACCAATTAATGGTCTCTAGGCTAATATT	803285
Qy	577	GTGGAAGGCAAGTCGTACTGTTCCGCTCGCCGACGAGCCACACGGTCAACTCCGAG	636
Db	803266	CATAACAGCAAGTGAAGCTATGAAAGCTTCCCAAGAAAGCAATACATCAACACTCCG	803325
Qy	637	TTGCACATCAAGCAGATCAGACGCTGCGCCCAAGGTGGAATCGCTACAGCTATAGGCAAC	696
Db	803326	TTTAAAGTAGAAAATAATAGATAGCTTACCCAAAGTGGGATTAATTATGCTTAATTCAAAT	803385
Qy	697	GTCAACGACACGGGCTTACAGGCGCTCGGACAGAAAGCGGCCCAAGGCGCTGATCAATGCC	756
Db	803386	GCACTCTGTGGAACCATTAACCCATTACTCAATGCTGGCTATCAAGGGAATTGATCTGCA	803445
Qy	757	GGCAACGGCAATGGCGTCGGGTGTCGCGGGGTGATGCCAGCCCTGACGAGAGCTGGCGCAAG	816
Db	803446	GGAGTTGGGAATGGAATAATGTAAATGTGCACACTTAAGATGCGCTAGAAAAAGCCGCAAA	803505
Qy	817	AACGCGCTGACAGATCAATTCGTTCTGTCACGTCACACAGGGCGGTTTCGTGTCGCTAACGCC	876
Db	803506	GATAGCGTCGTTGTATGTCCGTTCTTCTCGTGTACCAAGGGTTATACAATCGTACGCT	803585
Qy	877	GAGCAGCCCGACGACAGAACGACTGGGTCTGGTCCCAAGACTTGAACCCGCGAAGAGGCC	936
Db	803566	GAAGTGTGATGATAGTAATAATATATGGCTTTGTAGATCAAGTACTTAATCAACAGAAAGCC	803625
Qy	937	CGCATCTCGGCGCATGTGGCAATGACCAAGACCCAGAACAGCAAGAGCTGCAGCGCAATT	996
Db	803626	CGCGGCTCTCTTGCAATTAGCTTTAACTCAAACTAAAGATCCNAAGTAATTAACCAATAT	803685
Qy	997	TTCTGGGAATACTGATA 1013	
Db	803686	TTCGAAGACTTTAAGA 803702	

RESULT 12
US-09-643-990A-1
Sequence 1 An

Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Hemophilus Influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/09/643,990A
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:

Accession	Sequence	Position
Db	803506 GATAGCGGCGATTGATAGTCCGTTCTTCTCGTGTACCAACGGGTTATTAACAATCGTGAAGCT	803565
Qy	877 GAGCAGCCCGCAGCAGACAGACTGGGTGCTGGGCCACAGACTGAAACCCGACAAAGGCC	936
Db	803566 GAACTTGATGATAGTAATAATATGCGCTTGTACATCAGGATCTTTAAATCCACAAAGGCC	803625
Qy	937 CGCATCCCGGGGATGATGATGGTGCATGACCAAGGCCAAGCAGCAAGAGAGCTGCAGGCAATT	996
Db	803626 CGCGTGCTCTTGCATTATGCTTTAATCTCAACTAAGATCCNAAAGTAATTCACAAATAT	803685
Qy	997 TTCTGGGATACTGATA	1013
Db	803686 TTCGAAGACTTCTAAGA	803702

RESULT 13
US-09-543-681A-1219
; Sequence 1219, Application US/09543681A

```

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1219
LENGTH: 1041
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-1219

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Query Match	12.7%	Score 129;	DB 4;	Length 1041;
Best Local Similarity	47.2%;	Pred. No. 9.9e-19;		
Matches 464;	Conservative	0;	Mismatches 510;	Indels 9;
			Gaps	2

QY 29 CCAACGTGTATCTCTGGCCACCGCGGCACATCGCCGGCGCTGGCCGCACCGCCGCA 88

Db 68 CTAAATGTACAAATCCTCGCAATCGGGGGAACCATGCGAGGGGGTGTG---ACTGTGCA 124

QY 89 ACAGGCCACTTACCAAGCTGCGCAAGTTGGGTGTGCACAGCTGATTTCCGGCGTCCGG 148

Db 125 CTCTCTCAAGCTACACCCGACAGAAATATGAGCATTTAGATCACTGATTATCCGACTGT 184

QY 149 AGCTGGCCGACTCTGGCCCATATGGCGGGCGAGCGAGTGAATGCAGATGCGCTCCGAAAGCA 208

Db 185 AGGCAAAAAAGTGTCTAACTTAAACAGGCGAGCAAGTGTAAATATGTGGTGTGCAAGTA 244

QY 209 TCACCAACGACGACCTGTCTCAAGCTGCGCAACAGCGTGGCCGAGCTGGCCGACAGCATG 268

Db 245 TGAAGACCAAGTGTGTTAAACTGGCGATTAATAAT-----TAATACGATTTGTGATA 298

QY 269 ACGTGGATGGCATCGTCATCAACCCATGGCACCGACACCTGTGAAGAAAACGGCTACTTTT 328

Db 299 AAACAGACGGCTTTGTGTATTAACCATGGTACAGATACGATGAAGAGACCGCTATTTC 358

QY 329 TGAACCTGTGTGAAAAAGACCGACAGCCGATCGTGTGTGTGGTTCCATGTGCCCCCGCA 388

Db 359 TTGACTTAACACACAGCATGTAAAAAACGGGTGTGTATGTAGGGGCAATGTGGCCACGCA 418

QY 389 CCGCATGTCCGCGGACGGCATGTCTCAACTGTATCAACGCGGTGGCCGTGGCCAGCAACA 448

Db 419 CAGCATTAAGTGTGTATGTATTCATTAACTCTATTAATCCGTGTGTGGTGGCAAGTGATA 478

QY 449 AGGACTCGCGCGGCAAGGGCGTGTCTGTGTGACCATGAACGACGAGATTCAGTTCGCGGCGTG 508

Db 479 AAGACTTGAAAAATGTGTGTATTAAGTTACATGAATTAATTCAGTATCAGTGTGAAG 538

QY 509 ACGTAGCAAGTCGATCAACATCAAGACCGAAGCTTCAAGAGCGGCTGGGCGCCGCGTGG 568

Dc	539	ATGTTGCAAAATATAATACGACAGAAAGTGCAGACATTCAGCCGATTAATCAGAGTGTCTC	598
Qy	569	GCATGCGTGGGAAGGCAAGTCGTACTGTTCCGCTCGCGGCGCAAGGCGCACACGTCCTA	628
Db	599	AAGGTTATGTTCAATGATGTGTAAGTACCTATTACACTGCTGCAACACCGCGCCTGAGA	658
Qy	629	ACTCCGAGTTTGCACATCAAGCAGATTCAGACGCTCCGCCAGGTGGAACATGCGCTACAGCT	688
Db	659	AAGTTGCTTTGATAGTGCAGCAAAATTACCGAAATTACCAAAAGTAGATATTGTTTAACT	718
Qy	689	ATGCAACGTCACCGACACGGCTTACAAAGCCCTGCGACAGAAACGGCGCCAAAGGCGCTGA	748
Db	719	ATGCTAATGCATCTGAATTTACCGGCTAAAGGTTTATAGATTAACCACTTTAAAGGTATTG	778
Qy	749	TCCATGCGCGGACCGGCAATGAGTGCAGTGTGCTGCGCGGAGTGTGCGACGCCCTGCAGAGAC	808
Db	779	TTAATGCAAGGTGTGCGCAATGTAACCTTAATTTGCAATCTTAAATACTTTAGCTGATG	838
Qy	809	TGCGCAGAAACGCGCGTGCAGATCAATTGGTTCGTCACTCAACAGCGCGGTTTCGTGCTGC	868
Db	839	GTTGTAAAAAAGGTTGTTGTGTGTGTGTGTTCTCAAGTCGTTCGCGTTTGGAATTTACACAC	898
Qy	869	GTATACGCCGAGCAGACCCGACGACAAAGAACGACTGAGTGTGTGCGCCACGACCTGAAACCGGC	928
Db	899	AAATATGATGAAGTAGATGATGATGCAAAATATGAGCTTATTGCTTCAGAAAGCTTAAATCCAC	958
Qy	929	AGAAAGCCCGCATCTTGGCGATGTGTGCAATGACCAAGACCCAGGACGACGAAGAGCTGC	988
Db	959	AGAAAGCAAGGTGTTTATACAGTTATCTTTGACAGAAACAAAGATCTCCGACGATCC	1018
Qy	989	AGCGCATTTTCTGGGAATACTGA	1011
Db	1019	AAGAAACTTTGAAAAATATTTAA	1041

RESULT 14
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328

```

? GENERAL INFORMATION:
? APPLICANT: FLEISCHMAN, Robert D.
? APPLICANT: WHITE, Owen R.
? APPLICANT: PRASER, Claire M.
? APPLICANT: VENTER, John C.
? TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
? TITLE OF INVENTION: TUBERCULOSIS
? FILE REFERENCE: 24366-20007.00
? CURRENT APPLICATION NUMBER: US/09/103,840A
? CURRENT FILING DATE: 1998-06-24
? NUMBER OF SEQ. ID NOS.: 2
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2
?
? LENGTH: 4403765
?
? TYPE: DNA
?
? ORGANISM: Mycobacterium tuberculosis
?
? FEATURE:
?
? OTHER INFORMATION: CDC 1551
?
? OTHER INFORMATION: "n" bases at various positions throughout the sequence
?
? US-09-103-840A-2

```

Query Match	8.2%;	Score 83;	DB 3;	Length 4403765;
Best Local Similarity	54.8%;	Pred. No. 5.5e-08;		
Matches 164;	Conservative	0;	Mismatches 135;	Indels 0;
				Gaps 0;

Accession	Gene	Protein	Accession	Gene	Protein
QY 230	AGCTGGCAAGCAGGTCGCGAGTGGCCGACAGCAATGACGATGAGTACATCA	205	Db 1742101	ACCGAATAGCGCGCTGCAGTCAGAGGCAATTCGCGCGCGCAGATGGGGGTGCTCATCA	1742042
QY 290	CCCATGGCACCGAACCCCTGGAAAGAAACCGCGCTACTTTTGAACCTGTGGTGGAAAGACCG	349	Db 1742041	CTACCGGACCCGATACGCTGTGAAGAGCCGCTCTGTGCTGACCTTACCTATCGCGGTA	1741982

Qy	350	ACAGGCGGATGGTGGTGGATTCCAGTGGCGCCCGGACCGCATGTCCGCGACGGCA	409
Db	1741881	GCCGCGCGGTGTGTGACCGGGGCGATGCTACGCGCGCATGTCCCGCGCGCATGGCC	1741922
Qy	410	TGCTCAACTGTACACGCGGTGGCGCGGCGACGACACAGAGCTGGCGCGGCAAGGGCG	469
Db	1741821	CGGCGCAATCTTCGCGACGCGCTTGGGGTCGCGCGACCCAGCGCGCGGCACTTGGGG	1741862
Qy	470	TGCTGTGATGCATGACGACGAGATCCAGTCCGGGCGTGGAGTGGAGTGCATCAAC	528
Db	1741861	TGCTGTGATGTTTGGCGCGCGCGGTGTTCACGCTTTGGGCTCTCACAAGGTGGCCAAC	1741803

RESULT 15
119-09-103

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103.840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match	8.2%	Score 83	DB 3	Length 4411529
Best Local Similarity	5.8%	Pred. NO.	5.5e-08	
Matches 164	Conservative	0	Mismatches 135	Indels 0
				Gaps 0

QY	230	GGCTGGCAGCAGGGTGGCCGAGCTGGCCGACACATATGATCTGATGGCATGCTCATCA	289
Db	1741976	ACCGGATNAGCGCGCTGCACTGACGAGGACATTTCCGGCGCGCGACGATGGGGTGTATCA	1741917
QY	290	CCCATGGCACCAGACCCCTGGAGAAAACCGCTTATCTTTTGAACCTGTGGAAAAGACG	349
Db	1741916	CTCAGCGCACCGGATACGCTCCAGAAAGACCGCTGTGGCTGACCTCACTATGCGGATA	1741857
QY	350	ACAAAGCGGATGCTGTGGTTCATATGCGCCCGGACACCGCATATCCGCGCGACGGCA	409
Db	1741856	GCGCGCCGGTGTGTTAACCGGGGCGATGTCAGCGCGCGATGCCCCGCGCGCGATGAGCC	1741797
QY	410	TGCTCAACTGTACAAAGCGCGGTGGCCGTGGCCAGCAACAAGACTCGCGCGACAGGCG	469
Db	1741796	CGGCGAATCTTCGGGAGCGCGCTTGGGATCGCGCGACCCAGCGCGCCGGAACTCGGGG	1741737
QY	470	TGCTGTGACCATGAAGACGAGATCCAGTCCGGGCGTACGTGACGATTCATCAAC	528
Db	1741736	TGCTGTGATGTTTGGCGCGCGCGGTATTAAGCTTTTGGGCTGTGACAAAGGTGGCCAAAC	1741678

Search completed: March 22, 2005, 12:57:48
Job time : 227 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 21:10:06 ; Search time 180 Seconds
(without alignments)
955.881 Million cell updates/sec

Title: US-09-842-628-2
Perfect score: 1680
Sequence: 1 KEVENQGLKLVAVILATGST.....MVAMTKTQDSKELQRIHFEY 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1592.5	94.8	362	1	ASPO_PSEPK
2	1579.5	94.0	337	1	ASPO_PSEB7
3	1480.5	88.1	362	1	ASPO_PSEFL
4	1432.5	85.3	362	1	ASPO_PSEB8
5	1040.5	61.9	355	2	Q6PAL6
6	1037.5	61.8	331	1	ASPO_ACTGL
7	795	47.3	354	2	Q87479
8	786	46.8	348	2	Q8XC02
9	786	46.8	348	2	Q83085
10	785	46.7	348	2	Q8CVR4
11	782	46.5	352	2	Q8A446
12	772	46.0	348	1	ASG2_BCOLI
13	768	45.7	352	2	Q64NH4
14	767	45.7	378	2	Q7VBE4
15	766	45.6	354	2	Q6L134
16	761	45.3	348	2	Q8XG73
17	761	45.3	348	2	Q7CPT7
18	758	45.1	349	1	ASG2_HABIN
19	758	45.1	375	1	ASG2_BACSU
20	757	45.1	330	1	ASPG_WOLSU
21	749.5	44.6	345	2	Q8ZGB7
22	749	44.6	348	1	ASPG_ERWCH
23	748.5	44.6	345	2	Q6GCJ2
24	739.5	44.0	331	2	Q9PJ82
25	735	43.8	346	2	Q6QAP4
26	735	43.8	349	2	Q7WVK9
27	734	43.7	348	2	Q6QAP3
28	730	43.5	349	2	Q7VNV6
29	729	43.4	355	2	Q65GV3
30	717	42.7	330	1	ASPG_HBLPY
31	687	40.9	332	1	ASPG_HBLPY

32	685.5	40.8	347	2	Q7N6D9	Q7N6D9
33	681	40.5	347	2	Q8ZLD3	Q8ZLD3
34	679	40.4	347	2	Q6ZJ01	Q6ZJ01
35	679	40.4	347	2	Q63U26	Q63U26
36	631	37.6	379	2	Q83K77	Q83K77
37	600	35.7	333	2	Q7WRB6	Q7WRB6
38	594	35.4	351	2	Q63JL0	Q63JL0
39	592	35.2	333	2	Q7W2H6	Q7W2H6
40	557	33.2	367	2	Q8XZT9	Q8XZT9
41	552.5	32.9	349	2	Q6CZM5	Q6CZM5
42	550	32.7	356	1	ASG2_SCHPO	Q9UB7
43	550	32.7	356	1	ASG4_SCHPO	Q8TIF8
44	527	31.4	360	1	ASG3_SCHPO	Q8NCO
45	524	31.2	360	1	ASG1_SCHPO	P87015

ALIGNMENTS

RESULT 1
ASPO_PSEPK STANDARD; PRT; 362 AA.
ID ASPO_PSEPK
AC Q88K39;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glutamine-asparagine precursor (EC 3.5.1.38) (L-asparagine/L-glutamine amidohydrolase) (L-ASNase/L-GLNase).
GN Name=anab; OrderedLocustNames=PP2453;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160486;
OX (1)
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolony J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Knout H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Medler H., Lauber J., Stjepanovic D., Hohnselt J., Stratz M., Heim S., Kiewitz C., Eisen J.A., Timmls K.N., Duesterhoft A., Tuemmler B., Frazer C.M.;
RT Complete genome sequence and comparative analysis of the Pseudomonas putida KT2440.
RL Briveton. Microbiol. 4:799-808(2002).
CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3).
CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
CC -1- SUBUNIT: Homotrimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Periplasmic (by similarity).
CC -1- SIMILARITY: Belongs to the asparaginase 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
EMBL: A016783; AAN68065.1; -.
HSSP: P10182; 4PGA.
DR TIGR: PP2453; -.
DR InterPro: IPR004550; Asnase II.
DR InterPro: IPR006034; Asp/Glutamase.
DR Pfam: PF00710; Asparaginase; 1.
DR PRINTS: PR00139; ASNGNAB.
DR ProDom: PD003221; Asp/Glutamase; 1.
DR PROSITE: PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE: PS00917; ASN_GLN_ASE_2; 1.
KW Complete proteome; Hydrolase; Periplasmic; Signal.

FT SIGNAL 1 25 Potential.
 FT CHAIN 26 362 Glutamine-asparaginase.
 FT ACT_SITE 45 45 By similarity.
 FT ACT_SITE 125 125 By similarity.
 FT ACT_SITE 126 126 By similarity.
 FT ACT_SITE 198 198 By similarity.
 FT ACT_SITE 362 AA, 38608 MW, C33F185D817053F0 CRC64,
 SQ SEQUENCE

Query Match 94.8%; Score 1592.5; DB 1; Length 362;
 Best Local Similarity 94.1%; Pred. No. 9, 2e-90;
 Matches 317; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 KEVENQOKLANYVITATGTTIAGAGSAANSATYQAAKGVKDLIAGVELADLANVGE 60
 DB 26 KEAETQOKLANVITATGTTIAGAGSAANSATYQAAKGVKDLIAGVELADIANVGE 85
 QY 61 QVMQIASSEITDDILKLASSVAELADSVNGIVITHTDPTLEERAYPLINVEKDKRI 120
 DB 86 QVMQIASSEISNDLKLKGRVAELAESKVDGIVITHTDPTLEERAYPLINVEKDKRI 145
 QY 121 VVVGSRPGTAMSDGMLNYNAVAASNKDSRGKGLVTNDEIQSGDVSKEINIKTE 180
 DB 146 VVVGSRPGTAMSDGMLNYNAVAASNKDSRGKGLVTNDEIQSGDVSKEAVNIKTE 205
 QY 181 AFKSAMGPIAMVEGSKYFRLPAKHTVNSEFDIKQISLPQVDIAYSGVNTDTAYYA 240
 DB 206 AFKSAMGPIAMVEGSKYFRLPAKHTVNSEFDIKQISLPQVDIAYSGVNTDTAYYA 265
 QY 241 LAONGAKALIHAGTGVSSRVPLQELRNKGVQIITSSR-QQSGFVLRAAEOPDDKN 299
 DB 266 LAONGAKALIHAGTGVSSRVPLQELRNKGVQIITSSRQSGFVLRAAEOPDDKN 325
 QY 300 DWVAHDLPORAKILAMVAMTKTQDSKEIQRIFWFY 336
 DB 326 DWVAHDLPORAKILAMVAMTKTQDSKEIQRIFWFY 362

RESULT 2
 ID ASPQ_PSES7 STANDARD, PRT, 337 AA.
 AC P10182;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DB Glutamine-asparaginase (EC 3.5.1.38) (L-asparagine/L-glutamine
 amidohydrolase) (L-ASNase/L-GLNase) (PGA).
 GN Name=anb;
 OS Pseudomonas sp. (strain 7A).
 OC Bacteria; Proteobacteria.
 NC NCBI_TaxID=313;
 RN [1]
 RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94347759; PubMed=8068664;
 RA Lubkowetz J., Wlodawer A., Ammon H.L., Copeland T.D., Swain A.L.;
 RT "Structural characterization of Pseudomonas 7A glutamine-
 asparaginase.";
 RT Biochemistry 33:10257-10265 (1994).
 RN [2]
 RP SEQUENCE OF 1-26.
 RX MEDLINE=78080774; PubMed=619999;
 RA Holtenberg J.S., Ericsson L., Roberts J.;
 RT "Amino acid sequence of the diazooxonorleucine binding site of
 Acinetobacter and Pseudomonas 7A glutamine-asparaginase enzymes.";
 RT Biochemistry 17:411-417 (1978).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=97172924; PubMed=9020792; DOI=10.1021/bi961979x;
 RA Jakob C.G., Lewinski K., Lacomte M.W., Roberts J., Leboda L.;
 RT "Ion binding induces closed conformation in Pseudomonas 7A
 glutamine-asparaginase (PGA): crystal structure of the PGA-SO4(2-)-
 NH4+ complex at 1.7-A resolution.";
 RT Biochemistry 36:923-931 (1997).
 CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3).

CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the asparaginase 1 family.
 DR PDB; 1DJO; X-ray; A/B=8-337.
 DR PDB; 1DJP; X-ray; A/B=8-337.
 DR PDB; 3PGA; X-ray; 1/2/3/4=1-337.
 DR PDB; 4PGA; X-ray; A/B=1-337.
 DR InterPro; IPR004550; Asnase_II.
 DR InterPro; IPR006034; Asp/Glutamase.
 DR Pfam; PF00710; Asparaginase; 1.
 DR PRINTS; PR00139; ASNGLNAB.
 DR ProDom; PD003221; Asp/Glutamase; 1.
 DR TIGRFAMs; TIGR00520; asnase_II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 KW 3d-structure; Direct protein sequencing; Hydrolase; Periplasmic.
 FT ACT_SITE 20 20
 FT ACT_SITE 100 100
 FT ACT_SITE 101 101
 FT ACT_SITE 173 173
 FT CONFLICT 7 7
 FT CONFLICT 12 12
 FT STRAND 11 18
 FT HELIX 20 22
 FT STRAND 24 25
 FT TURN 28 29
 FT STRAND 34 35
 FT HELIX 41 46
 FT TURN 47 47
 FT TURN 49 50
 FT TURN 51 54
 FT HELIX 56 65
 FT STRAND 67 69
 FT HELIX 72 87
 FT TURN 89 90
 FT STRAND 93 97
 FT TURN 101 102
 FT HELIX 103 113
 FT STRAND 120 123
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 FT STRAND 196 199
 FT TURN 208 210
 FT HELIX 215 217
 FT STRAND 224 228
 FT TURN 231 232
 FT HELIX 236 243
 FT TURN 244 245
 FT STRAND 248 254
 FT TURN 255 257
 FT STRAND 258 258
 FT TURN 261 263
 FT HELIX 264 272
 FT TURN 273 274
 FT STRAND 276 281
 FT TURN 286 286
 FT TURN 291 293

O -> H (in Ref. 2).
 V -> R (in Ref. 2).

FT HELIX 297 300
 FT TURN 301 301
 FT STRAND 303 304
 FT TURN 306 307
 FT HELIX 310 320
 FT TURN 321 323
 FT HELIX 327 337
 SQ SEQUENCE 337 AA, 36200 MW, 11DEBC467CB1475B CRC64;

Query Match 94.0%; Score 1579.5; DB 1; Length 337;
 Best Local Similarity 94.1%; Pred. No. 5.3e-89;
 Matches 317; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

QY 1 KEVENOQKLANVYIATGTTAGAGASANSATYQAAXGVDPKLAGVELADLANVRC 60
 DB 1 KEVENOQKLANVYIATGTTAGAGASANSATYQAAXGVDPKLAGVELADLANVRC 60
 QY 61 QVMOJASBSITNDLLKASSVAELADSDVDGIYTHGTDLLETFAYELAVETKDKPI 120
 DB 61 QVMOJASBSITNDLLKASSVAELADSDVDGIYTHGTDLLETFAYELAVETKDKPI 120
 QY 121 VVVGSRPCTAMSADGMLNNAVAVASNKDSRGKGLVYTMDEIOSGRDVSINIKTE 180
 DB 121 VVVGSRPCTAMSADGMLNNAVAVASNKDSRGKGLVYTMDEIOSGRDVSINIKTE 180
 QY 181 AFKSAMGFLGMVVEGKSYWFRLPARKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKA 240
 DB 181 AFKSAMGFLGMVVEGKSYWFRLPARKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKA 240
 QY 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSR-QQGGFYLRNAEQPDDKN 299
 DB 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSR-QQGGFYLRNAEQPDDKN 299
 QY 300 DMVVAHDLPQKARILAMVAMTKTQDSKELQRFMEY 336
 DB 300 DMVVAHDLPQKARILAMVAMTKTQDSKELQRFMEY 336
 DB 301 DMVVAHDLPQKARILAMVAMTKTQDSKELQRFMEY 337

RESULT 3

ASPO_PSEFL STANDARD; PRT; 362 AA.
 ID ASPO_PSEFL 068897;

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutaminase-asparaginase precursor (EC 3.5.1.38) (L-asparagine/L-glutamine amidohydrolase) (L-ASNase/L-GLNase).

GN Name=ansb;
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=294;

RA Hueser A., Kloepper U., Roehm K.H.;
 RT "Cloning, sequence analysis, and gene expression of the P. fluorescens gene (ansb) encoding periplasmic glutaminase/asparaginase."
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3).
 CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: Belongs to the asparaginase 1 family.

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DR EMBL; AF056495; AAC33155.1; -.
 DR HSSP; P10182; 3PGA.
 DR InterPro; IPR004550; Asnase II.
 DR InterPro; IPR006034; Asp/Glutaminase.
 DR Pfam; PF00710; Asparaginase; 1.
 DR PRINTS; PR00139; ASNGINASE.
 DR ProDom; PD003221; Asp/Glutaminase; 1.
 DR TIGRFAMs; TIGR00520; asnase II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 KW Hydrolyase; Periplasmic; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 362 Glutaminase-asparaginase.
 FT ACT_SITE 45 45 By similarity.
 FT ACT_SITE 125 125 By similarity.
 FT ACT_SITE 126 126 By similarity.
 FT ACT_SITE 198 198 By similarity.
 SQ SEQUENCE 362 AA, 38735 MW, E8C640D24C5FP31B CRC64;

Query Match 88.1%; Score 1480.5; DB 1; Length 362;
 Best Local Similarity 87.2%; Pred. No. 6.8e-83;
 Matches 294; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 KEVENOQKLANVYIATGTTAGAGASANSATYQAAXGVDPKLAGVELADLANVRC 60
 DB 26 KEVENOQKLANVYIATGTTAGAGASANSATYQAAXGVDPKLAGVELADLANVRC 85
 QY 61 QVMOJASBSITNDLLKASSVAELADSDVDGIYTHGTDLLETFAYELAVETKDKPI 120
 DB 86 QVMOJASBSITNDLLKASSVAELADSDVDGIYTHGTDLLETFAYELAVETKDKPI 145
 QY 121 VVVGSRPCTAMSADGMLNNAVAVASNKDSRGKGLVYTMDEIOSGRDVSINIKTE 180
 DB 146 VVVGSRPCTAMSADGMLNNAVAVASNKDSRGKGLVYTMDEIOSGRDVSINIKTE 205
 QY 181 AFKSAMGFLGMVVEGKSYWFRLPARKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKA 240
 DB 206 AFKSAMGFLGMVVEGKSYWFRLPARKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKA 265
 QY 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSR-QQGGFYLRNAEQPDDKN 299
 DB 266 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSR-QQGGFYLRNAEQPDDKN 325
 QY 300 DMVVAHDLPQKARILAMVAMTKTQDSKELQRFMEY 336
 DB 326 DMVVAHDLPQKARILAMVAMTKTQDSKELQRFMEY 362

RESULT 4

ASPO_PSEFL STANDARD; PRT; 362 AA.
 ID ASPO_PSEFL 091407;

DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutaminase-asparaginase precursor (EC 3.5.1.38) (L-asparagine/L-glutamine amidohydrolase) (L-ASNase/L-GLNase).

GN Name=ansb; Ordered locus names=PA1337;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=287;

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Madman S., Yan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K.T., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sater M.H., Hancock R.R.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT opportunistic pathogen." ;
 RL Nature 406:959-964 (2000) .
 CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3) .
 CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3) .
 CC -1- SUBUNIT: Homotetramer (By similarity) .
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity) .
 CC -1- SIMILARITY: Belongs to the asparaginase 1 family .
 CC -----
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 CC or send an email to license@isb-sib.ch) .
 CC -----
 CC EMBL, AB004563; ANG04726.1; --
 DR PIR, C83478; C83478.
 DR HSP, P10182; 3PGA.
 DR InterPro: IPR004550; Asnase II.
 DR InterPro: IPR006034; Asp/Glutamase.
 DR Pfam: PF00710; Asparaginase; 1.
 DR PRINTS; PR00139; ASNGLNASE.
 DR ProDom: PD003221; Asp/Glutamase; 1.
 DR TIGRFAMs; TIGR00520; asnase II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 DR Complete proteome: Hydratase; Periplasmic; Signal.
 KM Complete proteome: Hydratase; Periplasmic; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 1 26 362 Glutaminase-asparaginase.
 FT ACT_SITE 45 45 By similarity.
 FT ACT_SITE 125 125 By similarity.
 FT ACT_SITE 126 126 By similarity.
 FT ACT_SITE 198 198 By similarity.
 FT SEQUENCE 362 AA; 38644 MW; 6158A98AD7981431 CRC64;
 SQ
 Query Match 85.3%; Score 1432.5; DB 1; Length 362;
 Best Local Similarity 84.3%; Pred. No. 5.9e-80;
 Matches 284; Conservative 22; Mismatches 30; Indels 1; Gaps 1;
 QY 1 KEVENQOKLANNVILATGTTAGAGASAAANSATYQAAKGVNDKLAGPELADLANVGE 60
 DB 26 KEVAQOKLSNVVILATGTTAGAGASAAANSATYAAKVPVQLLASVQLDIANVGE 85
 QY 61 QVMOJASISITDDLLKLASSVAELADSDVDGIYTHGTDTLBETAYFLNVEKTDKPI 120
 DB 86 QVFOJASISFTENLELTKYAKLADSDVDGIYTHGTDTLBETAYFLNVEKTDKPI 145
 QY 121 VVVGSMRPGTANASADQMLNLVNAVAASNKDSRGKGVLTVMNDEIQSGRDVSKSINIKTE 180
 DB 146 VVVGSMRPGTANASADQMLNLVNAVAASNKDSRGKGVLTVMNDEILSGRDAKMNINIKTE 205
 QY 161 AFKSAWGPGLGMVVEKSKYVFLPAKRTHTNSFPDIKQISLPOVDIAYSIGNVTYAYKA 240
 DB 206 AFKSPWGPGLGMVVEKSKYVFLPAKRTHTNSFPDIKQISLPAVIAVSIGNVSTAYKA 265
 QY 241 LAQNGAKLIIHAGTNGSVSRVVPALQELRKNGVQIIRSSR-QQSGFYLRNAEQPDDKN 299
 DB 266 LAQNGAKLIIHAGTNGSVSRVVPALQELRKNGVQIIRSSR-VNNAAGFYLRNAEQPDDKN 325
 QY 300 DWVAHADINPQKARILAMVAMTKTQDSKELQRIEMEX 336
 DB 326 DWVAHADINPQKARILAMVAMTKTQDSKELQRIEMEX 362
 RESULT 5
 Q6FAL6 PRELIMINARY; PRT; 355 AA.
 AC Q6FAL6;
 DT 05-JUL-2004 (TREMREL. 27, Created)
 DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
 DT 05-JUL-2004 (TREMREL. 27, Last annotation update)
 DE Glutaminase-asparaginase (EC 3.5.1.38) .

GN Name=aspg; OrderedLocuNames=ACIAD2088;
 OS Acinetobacter sp. (strain ADP1) .
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=62977;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Ozlas S.,
 RA Labarre L., Cruveiller S., Robert C., Duprat S., Wncker P.,
 RA Ormiston L.N., Weissenbach J., Marliere P., Cohen G.N., Médigue C.;
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.
 ADP1, a versatile and naturally transformation competent bacterium." ;
 RL Nucleic Acids Res. 0:0-0 (2004) .
 DR EMBL; CR543861; CAG68897.1; --
 DR GO; GO:0050417; F:asparaginase activity; IEA.
 DR GO; GO:0050417; F:glutamin-(asparagin-)-ase activity; IEA.
 DR GO; GO:0006520; P:amino acid metabolism; IEA.
 DR GO; GO:0006528; P:asparagine metabolism; IEA.
 DR InterPro: IPR004550; Asnase II.
 DR InterPro: IPR006034; Asp/Glutamase.
 DR Pfam; PF00710; Asparaginase; 1.
 DR PRINTS; PR00139; ASNGLNASE.
 DR ProDom: PD003221; Asp/Glutamase; 1.
 DR TIGRFAMs; TIGR00520; asnase II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 KM Complete proteome.
 SQ SEQUENCE 355 AA; 37925 MW; C007FB5751720C45 CRC64;
 Query Match 61.9%; Score 1040.5; DB 2; Length 355;
 Best Local Similarity 63.8%; Pred. No. 6.1e-56;
 Matches 210; Conservative 46; Mismatches 70; Indels 3; Gaps 2;
 QY 11 NVVILATGTTAGAGASAAANSATYQAAKGVNDKLAGPELADLANVGEQVMOJASISI 70
 DB 27 NVVAVATGTTAGAGASAAANSATYTAAPVADALINAVPQKDLANVSGIQALQJASISI 86
 QY 71 TNDLLKLASSVAELADSDVDGIYTHGTDTLBETAYFLNVEKTDKPIVVVGSMRPGT 130
 DB 87 TDKELLSLARGVNDLVKKPSVNGVYTHGTDTLBETAYFLNVEKTDKPIVVGSMRST 146
 QY 131 AMSADQMLNLVNAVAASNKDSRGKGVLTVMNDEIQSGRDVSKSINIKTEAPKSAWGPGL 190
 DB 147 ALSADQMLNLVNAVAASNKDSRGKGVLTVMNDEIFAPARDVTKGINITNAFVSGMGLG 206
 QY 191 NVVEGSKYVFLPAKRTHTNSFPDIKQISLPOVDIAYSIGNVTYAYKALQNGAKA 248
 DB 207 TLVBGKPYWFSVYGRHTNASEFNENIKQDQLPVOIVYSGDSMTIPALVIAKAKAKA 266
 QY 249 LIHAGTNGSVSRVVPALQELRKNGVQIIRSSRQGGFYLRNAEQPDDKNVVAHDL 307
 DB 267 IINAGTNGSVGNVIVPLTKKLHDEQGIQIIRSSRVPQGFYLRNAEQPDDQGVVVAHDL 326
 QY 308 NPQKARILAMVAMTKTQDSKELQRIEMEX 336
 DB 327 NPQKARILAMVAMTKTQDSKELQRIEMEX 355
 RESULT 6
 ASPQ_ACIGL STANDARD; PRT; 331 AA.
 AC ASPQ_ACIGL;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glutaminase-asparaginase (EC 3.5.1.38) (L-asparagine/L-glutamine
 DE amidohydrolase) (L-Asnase/L-Glnase) .
 GN Name=ansb;
 OS Acinetobacter glutaminasifigans.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=474;
 RN (1)

RP SEQUENCE.
 RX MEDLINE=88243706; PubMed=3379033;
 RA Tanaka S., Robinson B.A., Appella E., Miller M., Ammon H.L.,
 RA Roberts J., Weber I.T., Wlodawer A.,
 RT "Structures of amidohydrolases. Amino acid sequence of a glutaminase-
 asparaginase from *Acinetobacter glutaminasificans* and preliminary
 RT crystallographic data for an asparaginase from *Erwinia chrysanthemi*,"
 RL J. Biol. Chem. 263:8583-8591 (1988).
 RN [2]
 RN SEQUENCE OF 1-60.
 RX MEDLINE=78080774; PubMed=619999;
 RA Holtenberg J.B., Ericsson L., Roberts J.,
 RT "Amino acid sequence of the diazoxonolactone binding site of
 RT *Acinetobacter* and *Pseudomonas* 7A glutaminase-asparaginase enzymes,"
 RL Biochemistry 17:411-417 (1978).
 RN [3]
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX PubMed=1529349;
 RA Lubkowski J., Wlodawer A., Housset D., Weber I.T., Ammon H.L.,
 RA Murphy K.C., Swain A.L.,
 RT "Refined crystal structure of *Acinetobacter* glutaminasificans
 RT glutaminase-asparaginase,"
 RL Acta Crystallogr. D 50:826-832 (1994).
 CC -1- CATALYTIC ACTIVITY: L-glutamine + H(2)O = L-glutamate + NH(3).
 CC -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the asparaginase I family.
 CC PIR: A28063; A28063.
 DR PDB: 1AGX; X-ray; @=1-331.
 DR InterPro: IPR004550; Asnase II.
 DR InterPro: IPR006034; Asp/Glutaminase.
 DR Pfam: PF00710; Asparaginase; 1.
 DR PRINTS: PR00139; ASNGLNASE.
 DR PRODOM: PD003221; Asp/Glutaminase; 1.
 DR TIGRFAse: TIGR00520; asnase II; 1.
 DR PROSITE: PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE: PS00917; ASN_GLN_ASE_2; 1.
 KM 3D-structure; Direct protein sequencing; Hydrolase; Periplasmic.
 FT ACT_SITE 12 12
 FT ACT_SITE 92 92
 FT ACT_SITE 93 93
 FT ACT_SITE 165 165
 FT BINDING 122 122
 FT STRAND 3 8
 FT STRAND 10 10
 FT TURN 11 13
 FT TURN 23 24
 FT TURN 33 37
 FT HELIX 38 39
 FT TURN 41 42
 FT HELIX 43 46
 FT STRAND 48 52
 FT STRAND 57 57
 FT STRAND 59 61
 FT HELIX 64 78
 FT TURN 79 79
 FT TURN 81 82
 FT STRAND 85 89
 FT STRAND 92 94
 FT HELIX 95 105
 FT STRAND 112 115
 FT TURN 121 122
 FT TURN 124 125
 FT TURN 128 139
 FT HELIX 140 140
 FT TURN 142 143
 FT TURN 145 146
 FT TURN 149 153
 FT STRAND 154 155
 FT STRAND 156 159
 FT TURN 160 162

FT STRAND 164 165
 FT TURN 171 172
 FT STRAND 174 175
 FT STRAND 182 185
 FT TURN 186 187
 FT STRAND 188 191
 FT HELIX 200 202
 FT TURN 207 209
 FT STRAND 218 222
 FT TURN 229 229
 FT HELIX 230 236
 FT TURN 237 239
 FT STRAND 242 248
 FT TURN 249 251
 FT STRAND 252 252
 FT TURN 255 256
 FT HELIX 257 266
 FT TURN 267 268
 FT STRAND 271 276
 FT STRAND 283 283
 FT TURN 285 287
 FT HELIX 291 294
 FT TURN 295 295
 FT STRAND 297 298
 FT STRAND 300 300
 FT TURN 301 301
 FT HELIX 304 314
 FT TURN 315 317
 FT HELIX 321 328
 FT TURN 329 331
 SQ SEQUENCE 331 AA; 35485 MW; 70F1BF623B9B0D31 CRC64;

Query Match 61.8%; Score 1037.5; DB 1; Length 331;
 Best Local Similarity 62.0%; Pred. No. 8.6e-56;

Matches 204; Conservative 52; Mismatches 70; Indels 3; Gaps 2;

QY 11 NVVIATGTTGAGASANSATYQAAKGVNKLAGEVELADLANVRGEQVWQIASSEI 70
 DB 3 NVVIATGTTGAGASANSATYQAAKGVNKLAGEVELADLANVRGEQVWQIASSEI 62
 QY 71 TNDLLKLAASVVELADSNVDGIVITHTGDTLLEBTAYFLNVEKTRDIVVGSNRPQT 130
 DB 63 TDKEELSLARQVNDLVKPKSVGVVITHTGDTMEETAFPLNIVHTDKIVLVGSNRPQT 122
 QY 131 AMSADGMLNVAVAASKDSRGQVLYTMDEIQSGRDVSKSINIKTEAKSANGPLG 190
 DB 123 ALSADGPLNLVSAVALASNEAKNGVWVLNDSIFPAADVTKGINITHAFVSQMGALG 182
 QY 191 NVVEGKSWFRLPAKRHTVNSRFDIKOI--SLPOVDIAYSIGNVTDTPYKALAQNGAKA 248
 DB 183 TIVBGRPWFRSSVKKHTNSFNIKIQGDALPGVQIYSGDNMPDAIYQAPAKAGVKA 242
 QY 249 LIHAGTNGSVSSRVVPALELR-KNGVQIIRSSRQGGFVLRNAEQDPDKNDVVVAHDL 307
 DB 243 ITHAGTNGSMANVYLVPEVRKLDHGGGLIVSSSHVAGQFVLRNAEQDPDKYGTIAAHDL 302
 QY 308 NPQKARILLAMVAMTQDSKEQLQRIFWEX 336
 DB 303 NPQKARILLAMVAMTQDSKEQLQRIFWEX 331
 RESULT 7
 ID 087079 PRELIMINARY; PRT; 354 AA.
 AC 087079;
 DT 01-JUN-2003 (TREMblrel. 24, Created)
 DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Periplasmic L-asparaginase II.
 GN OrderedLocustNames-VPA0374;
 OS *Vibrio parahaemolyticus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrionaceae; Vibrionaceae; Vibrionaceae;

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OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3_K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nishida M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005085; BAC6171.1; -.
DR HSSP; P06608; IHG1.
DR GO; GO:0004067; P:asparaginase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006528; P:asparagine metabolism; IEA.
DR InterPro; IPR004550; Asnase_II.
DR InterPro; IPR006034; Asp/Glutamase.
DR Pfam; PF00710; Asparaginase; 1.
DR PRINTS; PR00139; ASNGINASE.
DR ProDom; PD003221; Asp/Glutamase; 1.
DR TIGRfam; TIGR00520; asnase_II; 1.
DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
DR Complete proteome.
SQ SEQUENCE 354 AA; 38004 MW; A1576A2EC3A6096 CRC64;

Query Match 47.3%; Score 795; DB 2; Length 354;
Best Local Similarity 48.2%; Pred. No. 6,8e-41;
Matches 160; Conservative 67; Mismatches 103; Indels 2; Gaps 2;

OY 6 CQKLVNVLATGTTAGAGAAASATYQAAKVGVDKLIAGVPELADLANVGEQVQOI 65
DB 24 QSDLENIKILAVGTTAGAGGATSS-NTAGKVGESLISAVPMSTNADISGEQVSI 82
OY 66 ASESTINDDLKLASSVAELADSNVDGIVITHTGDTLEETAYFLNVEKTKPIYVGS 125
DB 83 GSQDNMDWEVLKAKRVNELAQDDVDGIVITHTGDTLEETAYFLDLTVKSDKPVYVGA 142
OY 126 MRPGTMSADGMLNLYNAVAVANSKDSRGKGLVTMNDIEISGRDVSISINIKTEAFSA 185
DB 143 MRPSTMSADGVLNLYNAVATNDEDSKRGVAVMNDITFPAKDVTKNTTSVSTFQSP 202
OY 186 -WGLPMVVEGKSYWFRLEPAKHVTNSSEPDIKQISLPQVDIAYSGVNTDTAYALAQN 244
DB 203 NCGPIGVINSADAKQSPERKHTTETPDVSKMLTLPVGIYVYANASSLPVALYDA 262
OY 245 GAKALIHAGTNGSVSRVVPALQELRKNGVOIIRSSROGGFVLRNAEQPDDKNDVVA 304
DB 263 KEDGIVSAGVNGNLYHTVFDLEEKASKGDIYVVRSSRTPTGSTTLDAEIDDDKYGFAV 322
OY 305 HDLNPOKARIILAMVAMTKTQDSKELQRIWFEX 336
DB 323 GTLNPOKARILMLSLTQTKNYQDVQKMFQY 354

RESULT 8
O8XC2 PRELIMINARY; PRT; 348 AA.
AC O8XC2; Q7AAW;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Periplasmic L-asparaginase II.
GN Name=anb; OrderedLocuNames=ECs3833, z4302;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

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RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Hayek G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G.J., Mackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouls K.,
RA Apodaca R.A., Nantharajan T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohtsuki M., Kurokawa K., Iehi K., Yokoyama K.,
RA Han C.-G., Ohtsuo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AB005526; AAG5808.1; -.
DR EMBL; AP002563; BAB37256.1; -.
DR PIR; A98108; A98108.
DR PIR; D85953; D85953.
DR HSSP; P0805; IJTA.
DR HSSP; P10172; IAGX.
DR GO; GO:0004067; P:asparaginase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006528; P:asparagine metabolism; IEA.
DR InterPro; IPR004550; Asnase_II.
DR InterPro; IPR006034; Asp/Glutamase.
DR InterPro; IPR00577; FGcy_kin.
DR Pfam; PF00710; Asparaginase; 1.
DR PRINTS; PR00139; ASNGINASE.
DR ProDom; PD003221; Asp/Glutamase; 1.
DR TIGRfam; TIGR00520; asnase_II; 1.
DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
DR PROSITE; PS00445; FGcy_KINASES_2; UNKNOWN_1.
DR Complete proteome.
SQ SEQUENCE 348 AA; 36850 MW; A5204EBD00910013 CRC64;

Query Match 46.8%; Score 786; DB 2; Length 348;
Best Local Similarity 48.3%; Pred. No. 2.4e-40;
Matches 159; Conservative 59; Mismatches 107; Indels 4; Gaps 3;

OY 9 LANVTLATGTTAGAGAAASATYQAAKVGVDKLIAGVPELADLANVGEQVQIAS 68
DB 23 LPNTITLITGTTAGAGGATSS-NTAGKVGESLISAVPMSTNADISGEQVSI 81
OY 69 SITNDLKLASSVAELADSNVDGIVITHTGDTLEETAYFLNVEKTKPIYVGS 128
DB 82 DMNDVMTLAKKIN--TDCDKTDFVITHTGDTLEETAYFLDLTVKCDKPVVVGAMRP 139
OY 129 GTMSADGMLNLYNAVAVANSKDSRGKGLVTMNDIEISGRDVSISINIKTEAFSA-WG 187
DB 140 STMSADGPFNLNLYNAVTAADKASANRGVAVMNDITFPAKDVTKNTTSVSTFQSP 199
OY 188 PLGMVVEGKSYWFRLEPAKHVTNSSEPDIKQISLPQVDIAYSGVNTDTAYALAQNGAK 247
DB 200 PLGIYHNGKIDYQRPARKHTSDTPEVSKNELPKVGIYVYANASSLPVALYDAGD 259
OY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSSROGGFVLRNAEQPDDKNDVVAHD 307
DB 260 GIVSAGVNGNLYKSVFTLATPAKNGAVVRSSRPVPGATTQDAEVDADAKGFIASGTL 319
OY 308 NPQKARIILAMVAMTKTQDSKELQRIWFEX 336
DB 320 NPQKARVLLALQTQKDPQOIQIFQY 348

RESULT 9
O83085 PRELIMINARY; PRT; 348 AA.

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AC Q83085; Q7C019;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Periplasmic L-asparaginase II.
GN Name=anab; OrderedLocustNames=53157, SP2954;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AEO15308; AAN44435.1; -.
DR EMBL; AEO16988; AAP18259.1; -.
DR HSSP; P00805; IJJA.
DR HSSP; P10172; IAGX.
DR GO; GO:0004067; F:asparaginase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006528; P:asparagine metabolism; IEA.
DR InterPro; IPR004550; AsnASE_II.
DR InterPro; IPR006034; Asp/Glutamase.
DR InterPro; IPR000577; FGGY_kin.
DR Pfam; PF00710; Asparaginase; 1.
DR PRINTS; PR00139; ASNGINASE.
DR ProDom; PD003221; Asp/Glutamase; 1.
DR TIGRfam; TIGR00520; asnASE_II; 1.
DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
DR PROSITE; PS00445; FGGT_KINASES_2; UNKNOWN_1.
KM Complete proteome; Hydrolase.
SQ SEQUENCE 348 AA; 36805 MW; BE2058CF5A010397 CRC64;

Query Match 46.6%; Score 786; DB 2; Length 348;
Best Local Similarity 48.6%; Pred. No. 2.4e-40;
Matches 160; Conservative 59; Mismatches 106; Indels 4; Gaps 3;

QY 9 LANNVILATGTTAGAGAAASATYQAQKVGVDKLIAGVPELADIANVGRGQVMQIASE 68
DB LPNITTLATGTTAGGDSATKS--NTYAGKVGVENLVNAPOLKDIANVGEVNVIGSQ 81
QY 69 SITNDLLKLASSVAELADSNVDGIVYTHGDTTLEETAYFLNLVEKTKPIYVVGSMRP 128
DB DNMNDVWTLAKKIN--ACDCKTDGFIYTHGDTMETAYFLDLTYKCDKPPVMVGAMRP 139
QY 82 SITNDLLKLASSVAELADSNVDGIVYTHGDTTLEETAYFLNLVEKTKPIYVVGSMRP 128
DB DNMNDVWTLAKKIN--ACDCKTDGFIYTHGDTMETAYFLDLTYKCDKPPVMVGAMRP 139
QY 129 GTAMSDGMLNLYNAVAASNTDSRGKGLVTNNDLISGGRDYSKINIKTEAFKSA-WG 187
DB STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
QY 140 STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
DB STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
QY 188 PLGMVVGKSYWFRLLPAKRTVNSBPDIKQISLPQVDIAYSGVNTDTRAYKALAGNKA 247
DB PLGYIHNGKIDYQRTPARKRTSDTPFDVSKLNLPKVGIYVYNAASDLPAKALVDAGYD 259

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QY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSSROQGGFVLNNAEPDDKNDVVAHDL 307
DB 260 GIVSAGVGNGLYKSPFDLITRAKNGTAVASSRVPATTTQDAVDADKGFVASGTL 319
QY 308 NPQKARILLAMVAMTKTQDSKEIQRIFWEY 336
DB 320 NPQKARVLLQLVLTQKDPQQAQIFNQY 348

RESULT 10
Q8CVR4 PRELIMINARY; PRT; 348 AA.
ID Q8CVR4;
AC Q8CVR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE L-asparaginase II (BC 3.5.1.1).
GN Name=anab; OrderedLocustNames=c3543;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=06.HI / CPT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raske D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Blattner F.R., Perna N.T.;
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AEO16766; AAN81991.1; -.
DR HSSP; P00805; IJJA.
DR GO; GO:0004067; F:asparaginase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006528; P:asparagine metabolism; IEA.
DR InterPro; IPR004550; AsnASE_II.
DR InterPro; IPR006034; Asp/Glutamase.
DR Pfam; PF00710; Asparaginase; 1.
DR PRINTS; PR00139; ASNGINASE.
DR ProDom; PD003221; Asp/Glutamase; 1.
DR TIGRfam; TIGR00520; asnASE_II; 1.
DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
KM Complete proteome; Hydrolase.
SQ SEQUENCE 348 AA; 36881 MW; 71105BD8B007C559 CRC64;

Query Match 46.7%; Score 785; DB 2; Length 348;
Best Local Similarity 48.6%; Pred. No. 2.7e-40;
Matches 160; Conservative 58; Mismatches 107; Indels 4; Gaps 3;

QY 9 LANNVILATGTTAGAGAAASATYQAQKVGVDKLIAGVPELADIANVGRGQVMQIASE 68
DB LPNITTLATGTTAGGDSATKS--NTYAGKVGVENLVNAPOLKDIANVGEVNVIGSQ 81
QY 69 SITNDLLKLASSVAELADSNVDGIVYTHGDTTLEETAYFLNLVEKTKPIYVVGSMRP 128
DB DNMNDVWTLAKKIN--TDCDKTDGFIYTHGDTMETAYFLDLTYKCDKPPVMVGAMRP 139
QY 82 DNMNDVWTLAKKIN--TDCDKTDGFIYTHGDTMETAYFLDLTYKCDKPPVMVGAMRP 139
DB DNMNDVWTLAKKIN--TDCDKTDGFIYTHGDTMETAYFLDLTYKCDKPPVMVGAMRP 139
QY 129 GTAMSDGMLNLYNAVAASNTDSRGKGLVTNNDLISGGRDYSKINIKTEAFKSA-WG 187
DB STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
QY 140 STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
DB STSMASDGFPNLYNAVATADKASARGLVVMNDVLDGRDVTKTNTTVDVATFKSVNYG 199
QY 188 PLGMVVGKSYWFRLLPAKRTVNSBPDIKQISLPQVDIAYSGVNTDTRAYKALAGNKA 247
DB PLGYIHNGKIDYQRTPARKRTSDTPFDVSKLNLPEVGIYVYNAASDLPAKALVDAGYD 259
QY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSSROQGGFVLNNAEPDDKNDVVAHDL 307

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Db 260 GIVSAGVNGNLKYTFDTLATPAKNGTAIVSSRVPTGATTQDAEVDADKXGFVASGML 319
 QY 308 NPOKARIAMVAMTKQDSKELORIFWEX 336
 Db 320 NPOKARVILALITOTKDPQOIQOIFNOY 348

RESULT 11

08A446 PRELIMINARY; PRT; 352 AA.

AC 08A446; 01-JUN-2003 (TRMBLrel. 24, Created)
 DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
 DE L-asparaginase II.
 GN OrderedLocNames=B27257;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OC NCBI_TaxID=818;
 RN (1) _

RP SEQUENCE FROM N.A.

RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=2250858; PubMed=1263928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Hamrod J., Deng S., Carmichael L.K.,
 RA Ching H.C., Hooper L.V., Gordon J.I.;
 RL "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016937; AA077863.1; -.
 DR HSP; P06608; 1HG1.
 DR GO; GO:0004067; F:asparaginase activity; IEA.
 DR GO; GO:0006520; P:amino acid metabolism; IEA.
 DR GO; GO:0006528; P:asparagine metabolism; IEA.
 DR InterPro: IPR004550; Asnase II.
 DR InterPro: IPR006034; Asp/Glutamase.
 DR Pfam: PF00710; Asparaginase; 1.
 DR PRINTS; PR00139; ASNGINASE.
 DR ProDom: PD003221; Asp/Glutamase; 1.
 DR TIGRfam; TIGR00520; asnase II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 DR Complete Proteome.
 KW SEQUENCE 352 AA; 37752 MW; 187E34EFC82BFCDF CRC64;

Query Match 46.5%; Score 782; DB 2; Length 352;

Best Local Similarity 48.0%; Pred. No. 4,3e-40;
 Matches 157; Conservative 62; Mismatches 106; Indels 2; Gaps 2;

QY 11 NVVILATGTTIAGAGASAAASATYQAAKGVDKLIAGVELADLANVGEQVQIASESI 70
 Db 27 NHILATGTTIAGTSSATGT-SYTAGVAIGALDLDAVEIKDIANVTSEQIVRIGSDM 85
 QY 71 TMDDLKASSVAELADSDVDGIVITHTDPLEEFAVPLNVEKDKIVVVGMRPCT 130
 Db 86 NDEWLTLLAKKINELLKRPDIDGIVITHTDMEETFAVPLNVTSDKVVVVGMRPCT 145
 QY 131 AMSADGMLNLVNAVAVASNRKSGKGLVTNMEIQSGDVGKSNIKTEAFKSA-WGPL 189
 Db 146 ALSADGPLNLVNAVAVTAAKESKDGVLVAMGILIGASVVKMTVDVQTQAPNSGL 205
 QY 190 GNVGEGKSYWFLPAKRTVNSBFDIKISSLPQVDIAYSQNVDTATKALANGAKAL 249
 Db 206 GVLNKGKVCYNQITLKKTITTSQVFPDVKLTSLPKVGIIVSYGNIIEADMTPLNNGYKGI 265
 QY 250 IHAGNGSVSSRVVPALEAKNGVQIIRSSRQSGFLRAAEQDDKNDVVAHDLP 309
 Db 266 IHAGVNGNINHNIPEPSLIDARRKGIIVVSSRVPTGPTLDAEVDADKXGFVASGML 325
 QY 310 OKARIAMVAMTKQDSKELORIFWEX 336
 Db 326 NPOKARVILALITOTKDPQOIQOIFNOY 352

RESULT 12

ASG2_ECOLI STANDARD; PRT; 348 AA.

AC P00805; 21-JUN-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE L-asparaginase II precursor (EC 3.5.1.1) (L-asparagine amidohydrolase II) (L-Asnase II) (Colaspase).
 GN Name=aneb; OrderedLocNames=B2957;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=562;
 RN (1) _

RP SEQUENCE FROM N.A.

RX MEDLINE=90170867; PubMed=2407723;
 RA Jennings M.P., Beacham I.R.;
 RT "Analysis of the Escherichia coli gene encoding L-asparaginase II, aneb, and its regulation by cyclic AMP receptor and FNR proteins.";
 RL J. Bacteriol. 172:1491-1498(1990).
 RN (2) _

RP SEQUENCE FROM N.A.

RC STRAIN=K12; MG155;
 RX MEDLINE=9426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN (4) _

RP SEQUENCE OF 23-348.

RX MEDLINE=80135739; PubMed=6766894;
 RA Malta T., Matsuda G.;
 RT "The primary structure of L-asparaginase from Escherichia coli.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:105-117(1980).
 RN (5) _

RP PARTIAL SEQUENCE.

RX MEDLINE=80048329; PubMed=387570;
 RA Malta T., Morokuma K., Matsuda G.;
 RT "Amino acid sequences of the tryptic peptides from carboxymethylated L-asparaginase from Escherichia coli.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:1483-1495(1979).
 RN (6) _

RP ACTIVE SITE.

RX MEDLINE=77140944; PubMed=321449;
 RA Peterson R.G., Richards F.F., Handschumacher R.E.;
 RT "Structure of peptide from active site region of Escherichia coli L-asparaginase.";
 RL J. Biol. Chem. 252:2072-2076(1977).
 RN (7) _

RP SUBUNIT.

RX MEDLINE=73007901; PubMed=4561256;
 RA Greenleaf A.C., Wriston J.C. Jr.;
 RT "Chemical evidence for identical subunits in L-asparaginase from Escherichia coli B.";
 RL Arch. Biochem. Biophys. 152:280-286(1972).
 RN (8) _

RP ACTIVE SITE THR-34.

RX MEDLINE=91293312; PubMed=1906013; DOI=10.1016/0014-5793(91)80723-G;
 RA Harms B., Wehner A., Aung H.P., Roehm K.H.;
 RT "A catalytic role for threonine-12 of E. coli asparaginase II as established by site-directed mutagenesis.";
 RL FEBS Lett. 285:55-58(1991).

[9] MUTAGENESIS OF HISTIDINE RESIDUES.
RX MEDLINE=92394146; PubMed=1521538; RA Wehner A., Haas E., Jennings M.P., Beacham I.R., Deret C., Baet P., RA Roehm K.H.;
RT "Site-specific mutagenesis of *Escherichia coli* asparaginase II. None of the three histidine residues is required for catalysis." Eur. J. Biochem. 208:475-480 (1992).
RN [10] MUTAGENESIS OF TREONINE AND SERINE RESIDUES.
RX MEDLINE=93156534; PubMed=1287659; RA Ders C., Henseleing J., Roehm K.H.;
RT "Probing the role of threonine and serine residues of *E. coli* asparaginase II by site-specific mutagenesis." J. Protein Eng. 5:785-789 (1992).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=93165718; PubMed=8434007; RA Swain A.L., Jaskolski M., Housset D., Rao J.K.M., Wlodawer A.;
RT "Crystal structure of *Escherichia coli* L-asparaginase, an enzyme used in cancer therapy." J. Proc. Natl. Acad. Sci. U.S.A. 90:1474-1478 (1993).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT VAL-111.
RX MEDLINE=96305806; PubMed=8706862; DOI=10.1016/0014-5793(96)00660-6; RA Palm G.J., Wlodkowski J., Deret C., Schleper S., Roehm K.H., Wlodawer A.;
RT "A covalently bound catalytic intermediate in *Escherichia coli* asparaginase: crystal structure of a Thr-89-Val mutant." FEBS Lett. 390:211-216 (1996).
RN [13] CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- INDUCTION: By CAMP and anaerobiosis.
CC -1- PHARMACEUTICL: Available under the names Crastin (Bayer), Elapar (Merck), Kidrolase (Rhône-Poulenc) and Leunase (Kyowa). Also available as a PEG-conjugated form (Pegaspargase) under the name Oncaspar (Intron). Used as an antineoplastic in chemotherapy. Reduces the quantity of asparagine available to cancer cells.
CC -1- MISCELLANEOUS: Km = 1.15 x 10⁻⁵ M.
CC -1- MISCELLANEOUS: *E. coli* contains two L-asparaginase isoenzymes: L-asparaginase I, a low-affinity enzyme located in the cytoplasm, and L-asparaginase II, a high-affinity secreted enzyme.
CC -1- SIMILARITY: Belongs to the asparaginase I family.
CC -1- DATABASE: NAME=Worthington-biochem manual; WWW="http://www.worthington-biochem.com/ASPR/".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sdb.ch/announce/> or send an email to license@isb-sdb.ch).
CC
CC -----
CC EMBL, M34277; AAA24062.1; -
CC EMBL, M34234; AAA23445.1; -
CC EMBL, U28377; AAA69124.1; -
CC EMBL, U00096; AAC75994.1; -
CC PIR, A35132; XDRC.
CC
CC PDB, 1HO3; X-ray; A/B=23-348.
CC PDB, 1IHD; X-ray; A/C=23-348.
CC PDB, 1JAZ; X-ray; A/B=23-348.
CC PDB, 1JJA; X-ray; A/B/C/D/E/F=23-348.
CC PDB, 1NNS; X-ray; A/B=23-348.
CC PDB, 3ECA; X-ray; A/B/C/D=23-348.
CC PDB, 4BCA; X-ray; A/B/C/D=-.
CC ECHOBASE; EB0044; -
CC EcoGene; EG10046; anB.
CC InterPro; IPR004550; Asnase II.
CC InterPro; IPR006034; Asp/Glutamine.
CC Pfam; PF00710; Asparaginase I.
CC PRINTS; PR00139; ASNGLNASE.

[illegible]

FT	HELIX	34	36
FT	STRAND	38	38
FT	TURN	42	43
FT	STRAND	48	48
FT	HELIX	54	60
FT	HELIX	62	66
FT	TURN	67	67
FT	STRAND	69	78
FT	HELIX	80	82
FT	HELIX	85	97
FT	HELIX	98	101
FT	STRAND	104	108
FT	TURN	112	113
FT	HELIX	114	124
FT	STRAND	131	134
FT	TURN	140	141
FT	TURN	143	144
FT	HELIX	147	158
FT	TURN	159	159
FT	HELIX	161	163
FT	TURN	164	165
FT	STRAND	168	172
FT	TURN	173	174
FT	STRAND	175	178
FT	TURN	179	181
FT	STRAND	182	184
FT	STRAND	186	186
FT	TURN	190	191
FT	STRAND	193	195

	Query Match	46.0%; Score 772; DB 1; Length 348;
	Best Local Similarity	47.7%; Pred. No. 1.7e-39;
	Matches 157; Conservative	59; Mismatches 109; Indels 4; Gaps 3
Oy	9 LANVIATAGGTIAGAGSAANSATYQAARKGVDTLIGVPEPLADLANVRGEQVMQJASB	68
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Db	23 LPTNLTATGTTIAGGGDSATYS -NTYVGKGVENVLVNAAPOLKOIANVKGGQVVNIISQ	81
Oy	69 SITDDLLKLTAASSVAELADSNVDGIVITTHGDITLEETAYFLNLVEKTDKP.VVWGNSMP	128
	: :	
Db	82 DMNNNVMLTLAKKN--TDCDKTGPFVITHGDIIEBAFYFDLTLYVCCKP.VWVGAMGP	139
Oy	129 GTMSADGMLLNAAVAVASNKRSGKGVLVTMDEISGRDVSKSINIKTEAFPSKA-WG	187
	:	
Db	140 STMSADGPNLVNAVVTAAADKASNRGLVVMNDTVLDGRVYTKNTTVDATFYSVNIG	199

QY 188 PLGAVVEGKSWFRLPAKHTVNSFPDIKQISLPQVDIANSYGVNTDTAYALANQAK 247
 DB 200 PLGYTHNGKIDYQRTPAKHTDTPEDVSXKINLEPKVGVVYANASDLPAALADAGAD 259
 QY 248 ALIHGNGSGSSSVRVPALQELRNKGVQIIRSSPQGGFVLNMEQDDKMDWVAIDL 307
 DB 260 GIVSGVNGNGLYKSVFDTLATPAKTGAVNVRSSVPTGATTQDAEVDKAGFVASGTL 319

RESULT 13

Q64NH4 PRELIMINARY; PRT; 352 AA.

AC 064NH4 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE L-asparaginase II.
 GN ORFNames=BP4215;
 OS Bacteroides fragilis.
 OC Bacteriia; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YC446;
 RA Kuehara T., Yamashita A., Hiraoka H., Nakayama H., Toh H., Okada N.,
 RA Kuehara S., Hattori M., Hayashi T., Ohnishi Y.,
 RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
 RT inversions regulating cell surface adaptation."
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
 DR EMBL: AP006841; BAD50958.1; -
 SQ SEQUENCE 352 AA; 38157 MW; 3379BD95053877D1 CRC64;

Query Match 45.7%; Score 768; DB 2; Length 352;
 Best Local Similarity 47.1%; Pred. No. 3.1e-39;
 Matches 154; Conservative 60; Mismatches 111; Indels 2; Gaps 2;

QY 11 NVVILATGTTAGAGASANSATYQAAKGVGDKLAGVPELADLANVGEQMOJASBI 70
 DB 27 NIHILATGTTAGTGS-ATSTNYTAGQVAISTLLDAVELLDIANVGEQIVRLASQDM 85
 QY 71 TNDLKLASSVAELADSDVDGIVYTHGDTLLESTAYFLNVEKTDKPIVVGSMRPGT 130
 DB 86 SDEWLLIAKKTINQILKRPDIDGIVYTHGDTLLESTAYFLNVEKTDKPIVVGSMRPGT 145
 QY 131 AMSADGMLNLVNAVAVASNKDSRGKGLVTWMDIIOGRDYSKINIKTEAFKSA-WGFL 189
 DB 146 ALSADGPINLVNAVAVTAGAKESIGKGLVLANGLIAGASAIKMTYIDVQTFQAPNSGAL 205
 QY 190 GNAVSGKSVFRLPAKHTVNSFPDIKQISLPQVDIANSYGVNTDTAYALANQAKAL 249
 DB 206 GYIFNGKAYVQAPLKHHTQSVFDTLATPAKTGAVNVRSSVPTGATTQDAEVDKAGFVASGTL 319
 QY 250 IHAGTNGSGSSSVRVPALQELRNKGVQIIRSSPQGGFVLNMEQDDKMDWVAIDLNP 309
 DB 266 IHAGTNGSGSSSVRVPALQELRNKGVQIIRSSPQGGFVLNMEQDDKMDWVAIDLNP 325
 QY 310 OKARILAMVAMTKTQDSKELORIFWEX 336
 DB 326 QKSRVLLILGLTKTNDMKQIQOYFNEY 352

RESULT 14

Q7VIE4 PRELIMINARY; PRT; 378 AA.

AC 07VIE4 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE L-asparaginase (EC 3.5.1.1).
 GN Name=ansb; OrderedLocustNames=HH0662;
 OS Helicobacter hepaticus.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=32025;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 51449 / 3B1;
 RX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
 RA Suerbaum S., Josenhans C., Stenzenbach T., Dreescher B., Brandt P.,
 RA Bell M., Droege M., Fattmann B., Fischer H.-P., Ge Z., Hoerster A.,
 RA Holland R., Klein K., Koenig U., Macko L., Menz G.L., Nakamura G.,
 RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.,
 RT "The complete genome sequence of the carcinogenic bacterium
 RT Helicobacter hepaticus."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
 DR EMBL: AF017146; AAP77259.1; -
 DR HSBP; F06608; IHG1.

DR GO:GO:0004067; F:asparaginase activity; IEA.
 DR GO:GO:0016787; F:hydrolase activity; IEA.
 DR GO:GO:0006520; P:amino acid metabolism; IEA.
 DR GO:GO:0006528; P:asparagine metabolism; IEA.
 DR InterPro; IPR004550; Asnase II.
 DR InterPro; IPR006034; Asp/Glutamine.
 DR Pfam; PF00710; Asparaginase; 1.
 DR ProDom; PD003221; Asp/Glutamine; 1.
 DR TIGRFAMS; TIGR00520; asnase II; 1.
 DR PROSITE; PS00144; ASN_GLN_ASE_1; 1.
 DR PROSITE; PS00917; ASN_GLN_ASE_2; 1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 378 AA; 40858 MW; 45FDD24FB9F93FAA CRC64;

Query Match 45.7%; Score 767; DB 2; Length 378;
 Best Local Similarity 47.4%; Pred. No. 3.8e-39;
 Matches 157; Conservative 71; Mismatches 99; Indels 4; Gaps 3;

QY 8 KLVNVILATGTTAGAGASANSATYQAAKGVGDKLAGVPELADLANVGEQMOJASBI 67
 DB 50 KKPNIIVILATGTTAGAVDSQIKTGVNAGVISTVTLLEAVPOLQEIHIQOEQIANTIDS 109
 QY 68 ESTNDLKLASSVAELADSDVDGIVYTHGDTLLESTAYFLNVEKTDKPIVVGSMRPGT 127
 DB 110 ADMNDLWTLTAQRNKLLENPKIDGIVYTHGDTLLESTAYFLNVEKTDKPIVVGSMRPGT 169
 QY 128 PGTASADGMLNLVNAVAVASNKDSRGKGLVTWMDIIOGRDYSKINIKTEAFKSA-W 186
 DB 170 PSTAISADGPINLVNAVAVTAGAKESIGKGLVLANGLIAGASAIKMTYIDVQTFQAPNSGAL 229
 QY 187 GPLGAVVEGKSWFRLPAKHTVNSFPDIKQISLPQVDIANSYGVNTDTAYALANQAK 245
 DB 230 GDMGYILDGKVFYFPKPHPTTHSEFVRSIRSLPKVDIYYSYANDGLATAAOLANQ 289
 QY 246 AKALIHAGTNGSGSSSVRVPALQELRNKGVQIIRSSPQGGFVLNMEQDDKMDWVAIDL 305
 DB 290 TKGLVLAGSGAGSIHKHNDKMLKQGLIVVQSSRLNGLIVL-ASBADKLAFISGG 347
 QY 306 DLNPKARILAMVAMTKTQDSKELORIFWEX 336
 DB 348 DLNPKARILAMVAMTKTQDSKELORIFWEX 378

RESULT 15

O6LI34 PRELIMINARY; PRT; 354 AA.

AC 06LI34 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative periplasmic L-asparaginase II.
 GN Name=Y2787; OrderedLocustNames=PBPRB1174;
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2005, 10:20:21 ; Search time 702 Seconds
(without alignments)
8599.100 Million cell updates/sec

Title: US-09-842-628-1

Perfect score: 1014
Sequence: 1 aaggaagtcggaacacga.....ttctctggaatcgtatga 1014

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 297611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.*
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22: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1014	100.0	US-09-842-628-1	Sequence 1, Appl1
2	219	1133	US-09-773-260-3	Sequence 3, Appl1
3	189.2	1128	US-10-406-025-1	Sequence 1, Appl1
4	145.6	14.4	US-09-882-227-83	Sequence 83, Appl1
5	138	13.6	US-10-339-670-1	Sequence 1, Appl1
6	138	13.6	US-10-158-865-1	Sequence 1, Appl1
7	89.4	8.8	US-10-425-115-4132	Sequence 43132, A
8	82.6	8.1	US-10-029-386-22613	Sequence 22613, A
9	78.4	7.7	US-10-411-910A-221	Sequence 221, App
10	75.8	7.5	US-10-029-386-20582	Sequence 20582, A
11	74.6	7.4	US-10-282-122A-14804	Sequence 14804, A

12	72.2	7.1	960	19	US-10-472-928-4159	Sequence 4159, Ap
13	72.2	7.1	2162598	18	US-10-472-928-4979	Sequence 4979, Ap
14	70	6.9	2364	19	US-10-473-687-3	Sequence 3, Appl1
15	70	6.9	2718	18	US-10-738-986-15	Sequence 15, Appl1
16	69.4	6.8	1749	18	US-10-411-910A-218	Sequence 218, App
17	69.2	6.8	1605	15	US-10-259-165-297	Sequence 297, App
18	69	6.8	1314	15	US-10-156-761-1793	Sequence 1793, Ap
19	69	6.8	1758	18	US-10-411-910A-209	Sequence 209, App
20	69	6.8	9025608	15	US-10-156-761-1	Sequence 1, Appl1
21	68.6	6.8	779	16	US-10-029-386-20935	Sequence 20935, A
22	68.6	6.8	985	18	US-10-363-345A-31407	Sequence 31407, A
23	68.6	6.8	985	18	US-10-363-345A-31408	Sequence 31408, A
24	67.2	6.6	791	16	US-10-029-386-20494	Sequence 20494, A
25	67.2	6.6	828	16	US-10-029-386-25443	Sequence 25443, A
26	67	6.6	1512	18	US-10-425-115-150486	Sequence 150486, A
27	66.8	6.6	1859	18	US-10-425-115-150483	Sequence 150483, A
28	66.4	6.5	1725	18	US-10-411-910A-196	Sequence 196, App
29	66.4	6.5	9025608	15	US-10-156-761-1	Sequence 1, Appl1
30	65.4	6.4	1444	18	US-10-767-701-12575	Sequence 56, Appl1
31	65.4	6.4	2475	17	US-10-260-238-5598	Sequence 12575, A
32	65.4	6.4	2475	17	US-10-260-238-5598	Sequence 5598, Ap
33	65.4	6.4	2475	17	US-10-425-114-16619	Sequence 16619, A
34	65.4	6.4	64492	17	US-10-378-083-1	Sequence 1, Appl1
35	65.2	6.4	871	16	US-10-029-386-20422	Sequence 20422, A
36	65.2	6.4	1089	15	US-10-156-761-6834	Sequence 6834, Ap
37	65.2	6.4	1761	17	US-10-156-761-3138	Sequence 3138, A
38	65	6.4	1398	17	US-10-369-493-11934	Sequence 31934, A
39	65	6.4	1485	18	US-10-411-910A-267	Sequence 267, App
40	64.6	6.4	786	15	US-10-187-267A-32	Sequence 32, Appl1
41	64.6	6.4	36321	15	US-10-187-267A-1	Sequence 1, Appl1
42	64.4	6.4	1268	18	US-10-716-803-2	Sequence 2, Appl1
43	64.4	6.4	5392	18	US-10-716-803-1	Sequence 1, Appl1
44	64	6.3	1107	15	US-10-156-761-2234	Sequence 2274, Ap
45	64	6.3	1312	18	US-10-437-963-29396	Sequence 29396, A

ALIGNMENTS

RESULT 1
US-09-842-628-1
; Sequence 1, Application US/09842628
; Patent No. US2002064862A1
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, JOSEPH
; APPLICANT: MACCALLISTER, THOMAS W.
; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: FREEMAN, ABBIE G.
; TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
; TITLE OF INVENTION: ANTIVIRAL AND ANTICANCER THERAPY
; FILE REFERENCE: 023032/0108
; CURRENT APPLICATION NUMBER: US/09/842, 628
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 08/050, 482
; PRIOR FILING DATE: 1995-04-25
; PRIOR APPLICATION NUMBER: PCT/US92/10421
; PRIOR FILING DATE: 1992-12-04
; PRIOR APPLICATION NUMBER: DE P 4140003.8
; PRIOR FILING DATE: 1991-12-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Pseudomonas sp.
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1008)
US-09-842-628-1
Query Match 100.0%; Score 1014; DB 9; Length 1014;
Best Local Similarity 100.0%; Pred. No. 4,16-259;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAAAGTGAAGACAGAGAGAGTGGCCAACTGATGATCTGGCCACCGCGCGACC 60
 DB 1 AAGAAAGTGAAGACAGAGAGAGTGGCCAACTGATGATCTGGCCACCGCGCGACC 60
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 DB 61 ATGCGCGCGCGCTGGCGCCAGCGCGCGCCCAAGCGCCCACTTACAGAGCTGGCAAGTTGGC 120
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 DB 121 GTGCGAAGAGTGAATGCGCGCGCTGGCGCGAGCTGGCGCACTGGCCAAATGGCGCGCGAG 180
 QY 181 CAGGTGATGACAGATGCGCTCCGAAAGCATCACCAAGAGAGCTGCTCAAGCTGGCAAGC 240
 DB 181 CAGGTGATGACAGATGCGCTCCGAAAGCATCACCAAGAGAGCTGCTCAAGCTGGCAAGC 240
 QY 241 AGCGTGGCGAGCTGGCGCGCAAGCAATGACGTGATGATGATGATGATGATGATGATGATG 300
 DB 241 AGCGTGGCGAGCTGGCGCGCAAGCAATGACGTGATGATGATGATGATGATGATGATGATG 300
 QY 301 GACACCGCTGGAAGAAACCGCTACTTTTGAACCTGCTGGAAGAAACCGCAAGCGCGATC 360
 DB 301 GACACCGCTGGAAGAAACCGCTACTTTTGAACCTGCTGGAAGAAACCGCAAGCGCGATC 360
 QY 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 361 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 TACAAAGCGCGCGCGCTGGCGCGCAAGCAATGACGTGATGATGATGATGATGATGATG 480
 DB 421 TACAAAGCGCGCGCGCTGGCGCGCAAGCAATGACGTGATGATGATGATGATGATGATG 480
 QY 481 ATGAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
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 QY 541 GCGTTCAAGAGCGCGCTGGCGCGCGCTGGCGCGAGTGGTGAAGAGCAAGTGGTGGTTC 600
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 QY 721 CTGCGCAAGAGCG 780
 DB 721 CTGCGCAAGAGCG 780
 QY 781 TGGCG 840
 DB 781 TGGCG 840
 QY 841 TCAGCTCAACAGAGCG 900
 DB 841 TCAGCTCAACAGAGCG 900
 QY 901 TGGGTCGTGGCG 960
 DB 901 TGGGTCGTGGCG 960
 QY 961 ACCAAGAGCG 1014
 DB 961 ACCAAGAGCG 1014

RESULT 2
 US-09-773-260-3
 ; Sequence 3, Application US/09773260

Patent No. US20020102251A1
 GENERAL INFORMATION:
 APPLICANT: Donald L. Durden
 TITLE OF INVENTION: UTILIZATION OF MOLINELLA SUCCINOGENES
 ASPARAGINASE IN THE TREATMENT OF HUMAN
 HEMATOLOGIC AND AUTOIMMUNE DISEASE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/773,260
 FILING DATE: 31-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/094,435
 FILING DATE: 1998-06-09
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburton, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 234/274
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1133 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-773-260-3
 Query Match 21.6%; Score 219; DB 9; Length 1133;
 Best Local Similarity 52.8%; Pred. No. 3.7e-48;
 Matches 521; Conservative 0; Mismatches 460; Indels 6; Gaps 2;
 29 CCAAGTGTGATCTGTGCGCAACCGCGCGCAACATGCGCGCGCTGGCGCGCGCGCGCGCGCG 88
 DB 128 CCAAGTGTGATCTGTGCGCAACCGCGCGCAACATGCGCGCGCTGGCGCGCGCGCGCGCGCG 187
 QY 89 ACAAGCGCACTTACAGAGCG 148
 DB 188 AGAG---TAGTACTCTGTGAGCGAGTCAACGTTGATTAAGCTTCTTCAAGCGCGTCCCTG 244
 QY 149 AGTGGCGCGAGCTGGCGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
 DB 245 CCATTAAGAGCTTACCGCAACATCAAGGTTGAAGATTTCAAGCATTTGAGCTTCCCAAGAGA 304
 QY 209 TCACCAAGAGAGAGCTGTCAAGCTGCGCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 268
 DB 305 TGACGGGTAAAGTGTGCTTTAACTAGCGCAAGCGGTGTAAAGTGTCTCTGCGCAAAAAG 364
 QY 269 AGCTGATGAGCATGCTATCAACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
 DB 365 AGACCGAAGCGGTATATCAACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424
 QY 329 TGAACCTGTGGAAGAGCGCAAGCGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 388

Db 425 TCNACCTCAACGCTGAAAGCCAAAACCTGCTCCTTGTAGGCGCCATGCGTCCAGGCT 484
 Qy 389 CGGCGCATGTCGCGCGACGGGATGCTCAACCTGTACAAACCGCGCGCGCGGCGGACGACA 448
 Db 485 CTTCAAGAGTGTGTAGGCGCCCATGAACTCTATTAACCGCGTAAATGATGCGATCAACA 544
 Qy 449 AGGACTCGGCGCGCAAGGCGTGTCTGTGTGACATGAAACGACGATCACTCGGCGGTG 508
 Db 545 AAGCCTCTATTAAGAAAGGTGTGTATGTATGAAACGATGAGATTACGCGCGCAAG 604
 Qy 509 AGCTGACGAATGATCAACATCAAGACCGAACCTTTCAA--GAGCGCTGTGGGCGCGC 565
 Db 605 AAGCGACCAAGCTCAACACCGCATCATGTCATTTGCTTGGCCCAACACAGGTAA 664
 Qy 566 TGGGCAATGTGTGGAAGGCAAGTGTATGTTCCGCTGCGCGCGCAACCGCAACCG 625
 Db 665 TCGGCAAGTGTATTAATGGAAGTGAAGTATTCATCAATCGTTGCACTTCACACCC 724
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 Db 725 TTGCAAGTGAATTAATTAAGAAATGGAAGAACTCCCGAGAGTCAATTTCTTTAG 784
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RESULT 3
 US-10-406-025-1
 / Sequence 1, Application US/10406025
 / Publication No. US20030186380A1
 / GENERAL INFORMATION:
 / APPLICANT: No. US20030186380A1ozymes Biotech, Inc.
 / APPLICANT: Thomas, Michael D.
 / APPLICANT: Sloma, Alan
 / TITLE OF INVENTION: Methode for producing secreted polypeptides having L-asparaginase
 / TITLE OF INVENTION: activity
 / FILE REFERENCE: 10289.200-US
 / CURRENT APPLICATION NUMBER: US/10/406, 025
 / CURRENT FILING DATE: 2003-04-01
 / PRIOR APPLICATION NUMBER: US 60/369,192
 / PRIOR FILING DATE: 2002-04-01
 / NUMBER OF SEQ ID NOS: 8
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 1
 / LENGTH: 1128
 / TYPE: DNA
 / ORGANISM: Bacillus subtilis
 US-10-406-025-1

Query Match 18.7%; Score 189.2; DB 16; Length 1128;
 Best Local Similarity 50.2%; Pred. No. 2.9e-40;
 Matches 498; Conservative 0; Mismatches 488; Indels 6; Gaps 1;

Qy 20 AAGAGCTGGCAACGATGATCTGTGCAACGCGCGGCAACATCGCGCGGCTGGCGCA 79
 Db 143 AGGATTTGCCAAACATTAAATTTTATGCAAGAGAGGCAAGATGCTGTGCGATCAAT 202
 Qy 80 GCGCGGCAACAGCGCACTTACAGGCTGCCAAGGTTGGCTGCAAGCTGATTTCCG 139
 Db 203 CGAAAACCTCAACATGAAATTAAGCAGGTGTGTGCGCGTTGAATCACTGATGAG 262
 Qy 140 GGTGCGGAGCTGGCGCACTGGCCATGTGTGCGCGGCAAGGATGATGACATGGCCT 199
 Db 263 CAGTTCCAAATAAGAGCAATTCGCAAGTCAAGCGCGCAGAGATTTGTAACGTGGCA 322
 Qy 200 CGAAAGCATCAACACGACGACCTGCTAAGTGGCAAGCGCGTGGCGGCTGGCGCG 259
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 Qy 260 ACAGCAATGACGTGATGCAATGCTATCATCAACCATGCAACCGACCTTGAAGAAACG 319
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 Qy 380 GCGCGGCAACCGCAATGTCGCGCAACGCGATGCTCAACCTGTACAAACGCGTGG 439
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 Qy 440 CCAGCAACAGGACTTCGCGCGCAAGGCGGTGTGTGCAATGAACGACGATCAAT 499
 Db 563 CAGTGTCCCTGAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 622
 Qy 500 CCGGCGGTGACGTGACCAAGTGTATCATCAATCAACGCAAGCTTCAAGCGCTGG 559
 Db 623 CAGCCGATATGTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA 682
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 Db 683 TGGGCTTGTGCAACAAATGCAATGATGATATCTTAATTAATGATTAATCCGTAAG 742
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 Db 743 ATACGAAGACAGGATTTCTGTGTTTCTAATCTTATGATGAGTGGCGGATTAAT 802
 Qy 680 CTTACAGTATGCAACGTCAACGACGCGCTTACAGGCGCTTGGCAAGAACGCGCA 739
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RESULT 4
 US-09-882-227-83
 / Sequence 83, Application US/09882227

Publication No. US20030158396A1
 GENERAL INFORMATION:
 APPLICANT: Kleantous, Harold
 APPLICANT: Al-Garawi, Amal
 APPLICANT: Miller, Charles
 APPLICANT: Tomb, Jean-Francois
 APPLICANT: Oomen, Raymond P.
 TITLE OF INVENTION: Identification of Polynucleotides
 TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
 FILE REFERENCE: 06132/047002
 CURRENT APPLICATION NUMBER: US/09/882,227
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 08/902,615
 PRIOR FILING DATE: 1997-07-29
 NUMBER OF SEQ ID NOS: 638
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 83
 LENGTH: 1196
 TYPE: DNA
 ORGANISM: Helicobacter pylori
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (41)...(1132)
 US-09-882-227-83

Query Match 14.4% Score 145.6; DB 10; Length 1196;
 Best Local Similarity 50.5%; Pred. No. 1,1e-28;
 Matches 436; Conservative 0; Mismatches 419; Indels 9; Gaps 3;

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 248 ATCAAGAGCTTTGAGAGCTATCTTAAGCTTTTAAGAGCTTTTAAGAGGAG 307
 181 CAGGTATGAGATGCTCTCCGAAAGCATACCAAGAGAGCTGCTCAAGTGGCAAGC 240
 308 CAGATTTCTAATGAGCTCACAAGAGCATGAAGAGTATGTTCAAGCTCCGCAAA 367
 241 AGCGTGGCGGAGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 368 CGTGCCCAAGATTGCTATGATATAGCGGTATTTCAAGGCGTGTATCAAGCTGCGCAG 427
 301 GACACCTGAGAGAAACGCTACTTTTGAACCTGCTGGAAGAGCGGAGAGCGGATC 360
 428 GACATTTTGAAGAGAGCGCGATTTTAACTTAAGTTTAACTTAACTTAACTTAACTT 487
 361 GTGTGTGTGTTTCAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 488 GTGTGTGTGAGAGATGCTATGCTGCTTTTGAAGCGGAGATGGGCGCTTGAATTA 547
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 548 TATAATGCTGTAGGCTGCTCAATGAAAAAGTGCATTAAGGCGCTGTAGTGGTG 607
 481 ATGAAGAGAGATCCAGTCCGGGCGTGAAGTGAAGATCGATCAATCAAGAGCGAA 540
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 541 GCGTTCAAGAGC--GCGTGGGCGCGCTGGGCGATGTTGTGGAAGGCAAGTGTACTGG 597
 668 ACCTTTAAAGCCTTAATATAGCGCGGAGATAGGAGAGGTATATATAGGCAAAAGCGGCTAT 727
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 908 GTAGCGGCTGGGTTTAAAGGAGATGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
 835 GCTTGTGACGTCAACAGGCGGCT 858
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RESULT 5
 US-10-329-670-1
 Sequence 1, Application US/10329670
 Publication No. US20040018503A1

GENERAL INFORMATION:
 APPLICANT: Pletschmann et al.
 TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragm
 FILE REFERENCE: PB186P1
 CURRENT APPLICATION NUMBER: US/10/329,670
 PRIOR FILING DATE: 2002-12-24
 PRIOR APPLICATION NUMBER: US 09/643,990
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: US 08/487,429
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: US 08/426,787
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
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 LENGTH: 1830121
 TYPE: DNA
 ORGANISM: Haemophilus influenzae
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Query Match 13.6%; Score 138; DB 17; Length 1830121;
Best Local Similarity 48.5%; Pred. No. 2,7e-26;
Matches 474; Conservative 0; Mismatches 491; Indels 12; Gaps 3;

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DB 802735 ATCTGGCAACGGGGGTACCAATTCAGAGAACGGGCAAAAGTTCCGTAA--TTCTCG 802791
QY 100 TACGAGCTGCCAAGTTGGCGTGCACAAAGCTATGGCGGCGGCGGCGGCGGCGG 159
DB 802792 TATTAAGCTGACCAATTAAGTATTAATCTTAATTAAGCTGACGAAATGAAT 802851
QY 160 CTGGCCCAATGTCGGCGGCGGAGAGGTGATGACATGCTGCTCCGAAGATCAACAC 219
DB 802852 ATTGCAACATTAAGGTGAGAGAAATTTGTAATAATAGTTTCAAGACATGAATACGA 802911
QY 220 GACCTGCTCAAGCTGGCAAGACGCTGGCGGCGGCGGCGGCGGCGGCGGCGG 279
DB 802912 GTCTGGCTAAATCTGGCAAAAGCCATCAATGCTCAATGTAATGAATGACT-----GATGGA 802965
QY 280 ATCTGATCAACCCATGACGACGACCCCTGGAAGAAACCGCTACTTTTGAACCTCGT 339
DB 802966 TTTGCTATTAACCAATGATACATGATACATGAAAGACGCTTATTTCTTAATTAAC 803025
QY 340 GAAAAGACCAACCAAGCCGATCGTGGTGGTTCATGCGCGCGGCGGCGGCGGCGG 399
DB 803026 GTAAATATGTAATAACCGGTGTTCTGTTGGGGGCAATGCGTCTGCAACGAAATAAGT 803085
QY 400 GCCGAGCGCATGCTCAACCTGTACAGCGCGTGGCGGCGGCGGCGGCGGCGGCGG 459
DB 803086 GCTGATGCCCCATTAATCTTAATGCTGCTGTCGACGACGAAATAATCAAGT 803145
QY 460 GGCAAGGCGCTGCTGTGACCAATGACGAGATCCGATCCGCGGCGGCGGCGGCGG 519
DB 803146 GGTCTGTGTTTAAATGTCGCAATGAATTAAGTATGATGCTGCGGATGTAACAAA 803205
QY 520 TCGATCAATCAATCAACCAAGCCCTTCAAGAGCGC---CTGGGGCGCGCTGGCGATG 576
DB 803206 ACCAGTACGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 803265
QY 577 GTGGAAGCAAGTCTGATGCTGCTGCGCGCTGGCGGCGGCGGCGGCGGCGGCGG 636
DB 803266 CATTAACCAAAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 803325
QY 637 TTGCAATCAATCAATCAATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696
DB 803326 TTTAACTGAATAAATTAAGATGCTTACCCCAAGAGCAAAATCAATCAATCAAT 803385
QY 697 GTCAACGACGAGGCTTACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 756
DB 803386 GCACTGTGCAACATTAAGATGCTTACCAATGCTGCTGCTGCTGCTGCTGCTG 803445
QY 757 GGCACCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 816
DB 803446 GGAATGCGCAATGCAATGATGATGATGATGATGATGATGATGATGATGAT 803505
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DB 803506 GATAGCGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803565
QY 877 GAGCAGCCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 936
DB 803566 GAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803625
QY 937 CGCATCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 996
DB 803626 CGCGGCTCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 803685
QY 997 TTCTGGGAATGATGAT 1013
DB 803686 TTGGAAGACTTCTAAGA 803702

RESULT 6
US-10-158-865-1
Sequence 1, Application US/10158865
Publication No. US20040203093A1
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm
FILE REFERENCE: P8186P2C1D1
CURRENT APPLICATION NUMBER: US/10/158,865
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1830121
TYPE: DNA
ORGANISM: Haemophilus influenzae
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QY 160 CTGGCCAAATGTGGCGCGCGCAGCAGGTGATGCAGATCGCTTCGGAAGATCATCCAAAGAC 219

OTHER INFORMATION: EST HUMAN HIT: AL110383.1, EVALU8 0.006+00
OTHER INFORMATION: NT HIT: g14756466, EVALU8 0.006+00
US-10-029-386-22613

Query Match 8.1%; Score 82.6; DB 16; Length 990;
Best Local Similarity 47.2%; Pred. No. 5,6e-12;
Matches 364; Conservative 0; Mismatches 389; Indels 18; Gaps 3;

```
QY 5 AAGTGGAGACACGAGAGAGAGCTGGCCAACTGGTGTATCTTGGCCACCGGGCCGACCATCG 64
DB AAGAGAGACTGTATACGACATCGCTTAAAGAGCCGCGACAGAGGACATCGCCAAAGAG 871
QY 65 CCGGCGCTGGCGCCAGCGCGCCCAACAGCGCCACTACAGGCTTCCAAAGTTGGCTCG 124
DB AGCGCGCCCAAGGACATCGCCAGAGAGAGCGCCGCCAAGAAATGCCCAAGAGAGAGCGCG 811
QY 125 ACAAAGTATTTGCGCGCTGCGGAGCTGGCGCACTTGGCCAAATGCGCGCGAGAGAG 184
DB CCCACGCGATCGCCAGAGAGAGCGCGCCAGAGGATCGCCAGAGAGAGCGCGCGCCAGAG 751
QY 185 TGAT-----GAGATCGCGCTTCCGAAAGATACGAAAGAGACCTTGGCTCAAGCTGGCA 238
DB GCATTCGACGAGAGAGAGAGCGCGCCAGAGGATCGCCAAAGAGAGAGCGCGCCAGAG----- 697
QY 239 GCAAGCTGAGCGAGCTGGCGCCCAACAGCAATGACGTGATGGCATCGTCAATCCCATGGCA 298
DB 696 ---GATGCGCCAAAGAGAGAGCGCGCCAGAGGATCGCCAAAGAGAGAGAGCGCGCCAG 640
QY 299 CCGACACCTTGGAGAGAAACCGCTTCTTTTGAACCTTGTGAAAGAGAGAGAGAGAGAG 358
DB 639 TCGCCAAAC---GAGAGATCGCGCCCAAGAGATCGCAAGAGAGAGAGAGAGAGAGAGAG 583
QY 359 TCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 418
DB 582 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
QY 419 TGTACAAAGCGCGTGGCGCTGGCGCAACAGCAATCGCGCGCAAGAGAGAGAGAGAGAG 478
DB 522 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 463
QY 479 CCAATGAACGAGAGAGATCGAGTCCGCGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 538
DB 462 CCGCCCAAGGAGATCGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
QY 539 AAGCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
DB 402 AGAGAGATCGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
QY 599 TCGGCGCTGCGCGCCCAAGCGCCCAACAGTCACTTCCAGTTTGAATCAAGAGAGATCAGCA 658
DB 342 TCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
QY 659 GCTGCGCCAGAGTGAATCGCTTCAAGTATGAGCAAGTCAAGAGAGAGAGAGAGAGAGAG 718
DB 282 AGAGAGATCGCGCCCAAGGAGATCGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
QY 719 CCTTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 769
DB 222 AGCGCGCCCAAGGAGATCGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 172
```

RESULT 9

US-10-411-910A-221
Sequence 221, Application US/10411910A
Publication No. US20040209256A1
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2

SEQ ID NO 221
LENGTH: 1518
TYPE: DNA
ORGANISM: Chlamydomonas reinhardtii
US-10-411-910A-221

Query Match 7.7%; Score 78.4; DB 18; Length 1518;
Best Local Similarity 46.3%; Pred. No. 7,6e-11;
Matches 339; Conservative 0; Mismatches 381; Indels 12; Gaps 2;

```
QY 46 GCCACCGCGGACCATATCGCGCGCTGGCGCCAGCGCGCCCAACAGCGCCACTTACAG 105
DB 160 GCCCGCGGACACCATTCGCGTGGCCCGCCACCGCAAGCGCGCGCCCACTGAGAG 219
QY 106 GCTGCAAGTTGGGTGAGCAAGCTGATTTGCGCGCGCGCGCGAGAGAGAGAGAGAGAG 159
DB 220 CTGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 279
QY 160 CTGGCAATGTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 219
DB 280 GTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 339
QY 220 GACTGTCAAGCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 279
DB 340 AGCGCGCGCAAGCTGGCCACAGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399
QY 280 ATGTCATCACCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 339
DB 400 CTGTTGCGCGCGCGAGCTGACATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
QY 340 GAAAAGACCGCAAGCGCGAGCTGCGTGGTGGTTCATGAGCGCGCGCGCGAGAGAGAGAG 399
DB 460 GAGACACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
QY 400 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
DB 520 CCGGCGTGGTGGCCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 579
QY 460 GCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 519
DB 580 TGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
QY 520 TCGATCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 573
DB 640 GGCATCCCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 699
QY 574 GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 633
DB 700 GAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
QY 634 GAGTTGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 693
DB 760 ATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 819
QY 694 AACGTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
DB 820 CCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
QY 754 GCCGCGACCGCG 765
DB 880 ACCACCGCGCGC 891
```

RESULT 10

US-10-029-386-20582/c
Sequence 20582, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
EXPRESSION ANALYSIS TWO

FILE REFERENCE: ABOICA-X-2
 CURRENT APPLICATION NUMBER: US/10/029,386
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 34288
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 20582
 LENGTH: 926
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AP000552.1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
 OTHER INFORMATION: EST HUMAN HIT: AL110383.1, EVALUATE 0.006+00
 OTHER INFORMATION: NT HIT: G114756466, EVALUATE 0.006+00
 OTHER INFORMATION: SWISSPROT HIT: P28481, EVALUATE 1.006-10
 US-10-029-386-20582

Query Match 7.5%; Score 75.8; DB 16; Length 926;
 Best Local Similarity 44.9%; Pred. No. 3,5e-10;
 Matches 333; Conservative 0; Mismatches 402; Indels 6; Gaps 1;

29 CCAAGTGTGATCTTGGCCACCGGCGCATGCTGGCGGCGCTGGCGCGCGCGCA 88
 923 CCGATGAGAGACCCCTTACACGATCACTTAAAGAGAGCGCCACACACATCGCTAACG 864
 89 ACAGGCGCCACCTACAGGCGTGCAGTGGCGTGCAGAGCTGATGCGCGCGCGCG 148
 863 AGATATCTGTACACGATCGCTAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 804
 149 AGTGGCGCGACCTGGCCATGTGCGCGCGAGAGAGAGTGAATGCGCTTCGAAAGCA 208
 803 CCGCCACGCGATCGCCACAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 750
 209 TCACCAAGAGACCTGCTCAAGCTGCGCAAGAGTGTGCGCGCGCGCGCGCGCGCGCG 268
 749 CCGCCACGAGATTCGCGAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 690
 269 AGCTGATGCGATCGCTCAATCCATGCGACCGACCTGGAAGAAACCGCTCTTT 328
 689 AGGGGATGCGCAACAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 630
 329 TGAACCTGTGAGAAAGACCGAGAGCGAGTGTGCGTGTGCGTTCATGCGCGCGCGCA 388
 629 TCGCCAAAGAGAGCG 570
 389 CCGCATGTGCG 448
 569 AGAGAGAGCG 510
 449 AGAATCTGCG 508
 509 AGCG 450
 509 AGCG 450
 509 AGCG 450
 449 CCGAGGCG 390
 569 GCATGTGTGAGAGCGCAAGTGTGCTGTGCTGCGCTGCGCGCGCGCGCGCGCGCGCG 628
 389 GCATGTGTGAGAGCG 330
 629 ACTCGGATGCGATCAAGAGAGATCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 688
 329 CCAAGGAGAGCG 270
 689 ATGGCAAGTCAACGAGCG 748

DB 269 AGGAGCG 210
 749 TCGATGCG 769
 DB 209 CCGCCACG 189

RESULT 11

US-10-282-122A-14804

Sequence 14804, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl

APPLICANT: Wall, Daniel

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: E11TRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14804

LENGTH: 1191

TYPE: DNA

ORGANISM: Bordetella pertussis

US-10-282-122A-14804

Query Match 7.4%; Score 74.6; DB 17; Length 1191;
 Best Local Similarity 45.7%; Pred. No. 7.6e-10;
 Matches 306; Conservative 0; Mismatches 354; Indels 9; Gaps 1;

24 GCTGGCCAACTGTGATCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 83
 411 GCTGTGCGATGTGTATGCTTCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
 84 GCGCAAGCG 143
 471 GCAAGCG 530
 144 GCGGAGCTGCG 203
 531 CAGCG 590

QY 204 AAGCATCACCAAGACGACCTGCTCAAGCTGGCAAGAGGCGGACGCTGGCGGAG 263
 DB 591 CTCGAGAGTGTGACCAACGCTGCTCACTCTGCAATGCTGGCGGACCAAGTGAACGCT 650
 QY 264 CAATGACGTGATGGCATGCTCATCAACCATGAGCAACGCTGGAAGAAACCGCTTA 323
 DB 651 GGTGGTGGCGGGGATGCGCAACGCTTCAATGCTGGCGGCGGCTGCGCATGGGCA 710
 QY 324 CTTTGTGAACCTGCTGGAAAAAGACGCAAGCGGATGCTGCTGGTGGTTCCATGGCGCC 383
 DB 711 GTGCTGGCGGAGCCGACGATGCAAGAGGCGCGCGCTGATCGAATCATGAAAGCG 770
 QY 384 GGGCAACGCGC-----ATGCGCGCGAGCGCATGCTCAACCTGTAAAGCGCGGCG 434
 DB 771 CCGCGCGCGCGAGGTCGCGCATTCACCGACGCTGGTGGCGGCAAGCTGCTGGCGGCA 830
 QY 435 CGTGGCCAGCAACAGGACTGCGCGGCAAGGCGCTGCTGTGACCATGAAAGCAAGAT 494
 DB 831 CGCGCGGCGCACCGTCAAGGCGGCGCGGCGGCGGAGGAGCAATGATCTGACAT 890
 QY 495 CCAATGCGGGCGTGAAGTGAAGCAATGCAATCAAGACCGAAAGCTTCAAGAGCGC 554
 DB 891 CGAAGCGAGACCGCGGACGCGCTGCGCGCATATCTCAAGAGCGCGGCGACATGCTG 950
 QY 555 CTGGGGCGCGCTGGGATGCTGTGAGGAGCAAGTGTCTGCTGCTGCGCGCGGCA 614
 DB 951 GAACGCTCGGCTGGGCTTTGATTCACAGCATGCTGCGCGGACGAGGTGGTGC 1010
 QY 615 GCGCCACAGTCACTCCGATTCGACATCAAGCATGACAGGCTGCGGAGTGA 674
 DB 1011 GGGCGCGCATGCGGACGCTGGCGGCGCTTTGATGTCGCGGCGGAGATACGCTGGCGG 1070
 QY 675 CATGCGCTA 683
 DB 1071 CATGCGCAA 1079

RESULT 12

US-10-472-928-4159
 ; Sequence 4159, Application US/10472928
 ; Publication No. US20050020813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
 ; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: P026926WO
 ; CURRENT APPLICATION NUMBER: US/10/472,928
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: GB-0107658.7
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 4979
 ; SOFTWARE: SeqMin99, version 1.03
 ; SEQ ID NO 4159
 ; LENGTH: 960
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 ; US-10-472-928-4159

Query Match 7.1%; Score 72.2; DB 19; Length 960;
 Best Local Similarity 53.3%; Pred. No. 3.2e-09;
 Matches 152; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 266 ATGACGTGATGATGCTGCTCATCAACCATGAGCAACGCTGGAAGAAACCGCTACT 325
 DB 221 ATTAACATGATGATGATGATGATCAACAGGAACCATATCTTAAGAGAAACGCTATT 280
 QY 326 TTTTGAACCTGCTGGAAGAAAGACGACACCGATGCTGCTGGTTCATGCGCGCG 385
 DB 281 TCTTGATATCAATGAGAGTTCCCATATGCTCTTCAACAGGAGCATGCGAGCT 340
 QY 386 GCACGCGCATGTCGCGGCGGATGCTCAACCTGTACAGCGCGCTGGCGGACAGA 445

DB 341 CCAATGAGCTCGTAGTAGTGTGTTTAAATTAACCTTAAGTCTTACGATGGCCAGC 400
 QY 446 ACAAGACTCGGCGGCAAGGCGTGTGTGATCAATGAGACGATCCAGTCCGGC 505
 DB 401 ATGACAGGGCTGCTGACAAAGAGTTTGTGTGTTAAGATGAATTCACGCTGCCA 460
 QY 506 GTGACGTGAGCAAGTGCATCAATCAACAGACGAAAGCTTCAAGA 550
 DB 461 AGTATGTACCAAAACATACATGACTAATGTACGACCTTCCAGA 505

RESULT 13

US-10-472-928-4979
 ; Sequence 4979, Application US/10472928
 ; Publication No. US20050020813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
 ; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE: P026926WO
 ; CURRENT APPLICATION NUMBER: US/10/472,928
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: GB-0107658.7
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 4979
 ; SOFTWARE: SeqMin99, version 1.03
 ; SEQ ID NO 4979
 ; LENGTH: 2162598
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 ; US-10-472-928-4979

Query Match 7.1%; Score 72.2; DB 19; Length 2162598;
 Best Local Similarity 53.3%; Pred. No. 8.1e-09;
 Matches 152; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 266 ATGACGTGATGATGCTGCTCATCAACCATGAGCAACGCTGGAAGAAACCGCTACT 325
 DB 1794585 ATTAACATGATGATGATGATGATCAACAGGAACCATATCTTAAGAGAAACGCTATT 1794644
 QY 326 TTTTGAACCTGCTGGAAGAAAGACGACACGCGATGCTGCTGGTTCATGCGCGCG 385
 DB 1794645 TCTTGATATCAATGAGAGTTCCCATATGCTTATCAAGAGGACATGCGTACT 1794704
 QY 386 GCAAGCGCATGTCGCGGCGGACGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
 DB 1794705 CCAATGAGCTCGTAGTAGTGTGTTTAAATTAACCTTAAGTCTTCAAGAGGCGG 1794764
 QY 446 ACAAGACTCGGCGGCAAGGCGTGTGTGATCAATGAGACGAGATCCAGTCCGGC 505
 DB 1794765 ATGACAGGGCTGCTGACAAAGAGTTTGTGTGTTAAGATGAATTCACGCTGCCA 1794824
 QY 506 GTGACGTGAGCAAGTGCATCAATCAACAGACGAAAGCTTCAAGA 550
 DB 1794825 AGTATGTACCAAAACATACATGACTAATGTACGACCTTCCAGA 1794869

RESULT 14

US-10-473-687-3
 ; Sequence 3, Application US/10473687
 ; Publication No. US20040133942A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miles, Paul
 ; APPLICANT: Kramer, Vance
 ; APPLICANT: Shen, Zhicheng
 ; APPLICANT: Shotkoski, Frank
 ; APPLICANT: Warren, Greg
 ; TITLE OF INVENTION: Novel Pesticidal Toxins
 ; FILE REFERENCE: S-6000PCT
 ; CURRENT APPLICATION NUMBER: US/10/473,687
 ; CURRENT FILING DATE: 2003-09-27
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 3
; LENGTH: 2364
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2364)
; OTHER INFORMATION: Maize optimized v1p3B
US-10-473-687-3

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```

Query Match      6.9%; Score 70; DB 18; Length 2364;
Best Local Similarity 45.5%; Pred. No. 1.4e-08;
Matches 327; Conservative 0; Mismatches 385; Indels 6; Gaps 2;

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QY 13 AACGACGAAAGCTGGCCAAAGTGTGATCTGGCCACCGGGGACCATCGCCGCGCT 72
DB 916 ATCATGAAAGACACTCGACAAAGAGAGAGAGTTCGGGTGAACATCTCCGAC 975
QY 73 GCGGCGAAGCGCGCCAAAGCGCCACTTACAGGCTGGCCAGTTGGCGTGCACAAAGCTG 132
DB 976 CTCTCCAAACCTTCTCCAAACCGGAACCTACGCAAGGCGCAAGGCTCCAAAGAGAGCGCC 1035
QY 133 ATTGCGGCGTGGCGGAGCTGGCCCACTTGGCCCAATGTGCGGGGAGAGAGTGAATGACG 192
DB 1036 AAGATCATCTGTGAGAGCGCAAGCGCGCTACGCTCTGTGGGCTTGAAGATGTCCAAAGAC 1095
QY 193 ATGCGCTCGAAGAAAGATCAACAAGACGACTGTCTCAAGCTGGCAAGAGCGTGGCCGAG 252
DB 1096 TCCATACACCGTGTCTAAGGCTTACAGAGCCAAAGCTTCAAGAGAGATACCAAGGTGACAA 1155
QY 253 CTGGCGCAAGCAATGACGTGATG--CATGTGTATCACTCATGGACCGACACCTG 309
DB 1156 GACTCCCTCTCGAATGCTGTACGCGACATGACCAAGCTCTCTGCGCCGACCAAGTCC 1215
QY 310 GAAAGAAACCGCTACTTTTGAACCTCTGTGAAAAAACCAGAACCGCATCTGTGTGTC 369
DB 1216 GAGCAATCTTACTTACCAACAACATCGCTTCCGAAAGATGATGATCAACAAGATC 1275
QY 370 GATTCCATGCGCGCGCGGACCGCCATGTCCGCGACGCGATCTCAACTGTACAAAGCC 429
DB 1276 ACCTTCAACCAAGAAATGAATCTCTCGGTACAGAGCCACCGCACTTCTACAGATCC 1335
QY 430 GTGGCGTGGCGCAAGCAAGGACTTCGCGCGCAAGGCGGTGTCGTGACATGAAACGAC 489
DB 1336 TCCACCGGCGACATGACCTTCAACAAGACCAAGTGAAGTCTCCGAGGCGCAATATCC 1395
QY 490 GAGATC---CACTCCGCGCGGTGACGTGAGCAATGATCAATCAAGACCGAAGCTTC 546
DB 1396 ACCCTCTCGCTTCAACCGACGCGGTGTACATGCGGTGCAATCTTCCGAGACCTTC 1455
QY 547 AAGACGCGCTGGGGGCGCGGTGAGTGTGTGAAGCAAGTGTGATCTGTTCGCGCTG 606
DB 1456 CTCACCCCGATCAAGGCGCTTGGCATGTGTGTGAGAGAACTTCAAGTCTGTGAACCTTC 1515
QY 607 CCGGCGAAGCGCGACACGCTCACTCCAGTTGACATCAAGCAAGTCAAGACCTTGCCC 666
DB 1516 ACCTCAAGTCTTACTCTCGGAGGTGCTCTGCGCAACGACCTCTCAACAAGAGAAC 1575
QY 667 CAGGTGACATGCGCTTACAGCTATGTGCAACGACCGGCTTACAAAGGCGCTG 724
DB 1576 AAGCTCATGTGCGCGCGCATGCGCTTCAATCTCCAACTGTGAGAAAGCGCAACCTG 1633

```

RESULT 15

```

; Sequence 15, Application US/10738986
; Publication No. US20040209241A1
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary
; APPLICANT: Geall, Andrew
; APPLICANT: Mloeh, Mary Kopke
; TITLE OF INVENTION: Codon-Optimized Polynucleotide-Based Vaccines Against Human
; CYTOMEGALOVIRUS INFECTION

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; FILE REFERENCE: 1530.0580001
; CURRENT APPLICATION NUMBER: US/10/738.986
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,549
; PRIOR FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: codon-optimized sequence of hCMV gB
US-10-738-986-15

```

```

Query Match      6.9%; Score 70; DB 18; Length 2718;
Best Local Similarity 44.8%; Pred. No. 1.4e-08;
Matches 357; Conservative 0; Mismatches 430; Indels 9; Gaps 2;

```

```

QY 15 CCAGCAAGCTGGCCAAAGTGTGATCTGGCCACCGGCGGACCATCGCGGCGTGG 74
DB 1776 CCAAGTGGGCGAGGACAAAGATCTGTGGGCAACCAAGAGACGAGATGACACT 1835
QY 75 GCGCAGCGCGCCAAAGCGCCACTTACAGAGCTGCCAAGTTGGCTTCAAGCTGAT 134
DB 1836 GCCCAGCTTGAAGATCTTATCGCGCAAGCGCTTACAGATAGTGAAGTACTGTT 1895
QY 135 TGCGGCGTGGCGGAGCTGGCGGACCTGGCCAAATGTGCGCGGAGAGATGACAGT 194
DB 1896 CAAGAGATGATCACTGAGAGACATGACACCTGAGACAGATATGCGCTGACAT 1955
QY 195 CGCTCCGAAAGATCAACCAAGACGACTGTCAAGTGGCGAAGAGCTGGCGGAGCT 254
DB 1956 GACCCCTTGAGAAACACGCACTTACAGGCTGTGAGCTGTA---CAAGCAAGAGAGCT 2012
QY 255 GCGCAGCAGATGACGTGTGATGATGATGATCATACCATGAGCAACCTGGAAGG 314
DB 2013 GAGAGCAGCAACGTTTGAACCTGTGAGAGAGATCAATGAGGAGTTCAACAGTACAGCA 2072
QY 315 AACGCTACTTTTGAACCTGTGAGAAAGAACGCAAGCGCATGTGTGTGCTTC 374
DB 2073 GAGGTGAAGTACTGTGAGAGACAGATGTGTGACCCCTGCCCCCTTACTGAAGGCTT 2132
QY 375 CATGCGCCCGGACACCGCATGTCCGCGACGCGCATGTCTCAACCTGTACAAAGCGCTG 434
DB 2133 GAGCAGACTGATGAGCGCGCTGTGGCGCGCGCAAGGCGGTGGCGGTGACATGCGGCG 2192
QY 435 CGTGGCCAGCAAGAGCTGCGCGGCAAGGCGTGTGTGACCAATGAAGAGAGAT 494
DB 2193 CGTGGCGGCGCGCGGTGACAGCGGTGTGAGAGGCGGTGCAACCTTCTGAAGAACCCCTT 2252
QY 495 CCAATCGCGGCGGTGACGTGAGCAAGTGCATCAACATCAAGACCGAAGCTTCAAGAGCG 554
DB 2253 CGGCGCTTTCACATCATCTCTGTGTGTGACATGCGCGTGTGATCATCACTTACTGATCTA 2312
QY 555 CTGGGCGCGGTGGCATGTGTGTGAAGGCAAGTGTGATCTGTTCGCGTGGCGCA 614
DB 2313 CACCAAGGAGAGAGGCTGTGACACCAAGCCCTGAGAAACCTGTTCCCTTACTGTGAG 2372
QY 615 GCGCAGCAGGTCACTCCGAGTTGACATCAAGAGATCAAGAGCTGCCCGCAGGTGA 674
DB 2373 CGCCGACGCGACACCGTGAACAGCGGAGAGACCAAGAGACCAAGACCTGCG----AGGC 2426
QY 675 CATGCGCTTACAGCTATGAGCAAGTCAACGACAGGCTTACAAAGGCGCTTGCACAAAGCG 734
DB 2427 CCCCCCAGCTTACAGAGAGAGCTGTACAAAGCGGAGAGAGGCCCCCGCCCCCAG 2486
QY 735 CGCCAGGCGCTGATCATGTCCGCGACCGGCAATGCTGTGTGTGCGCGGAGGTGCC 794
DB 2487 CAGGAGCGCAGCAACCGCGCGCCCCCTTACACCAAGAGAGGCTTACAGATGCTGCT 2546
QY 795 AGCTTGCAGAGAGCTG 810

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Db 2547 GGCCCTGGCCAGGCTG 2562

Search completed: March 22, 2005, 13:09:36
Job time : 713 secs

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D	b635	CATCGCGGGCCCGGCGGCCCAAGCCGCCCANACGCCCACTTACACACCGCGCCAAAGTGCC	576
Oy	120	CGTCGAACAAGTTGATTGCOCGCGTGCCGAGCTGGCCGACTTGGCCAATGTGCGCGCGA	179
D	575	GGTGGAACAAGTTGGCTGGCCACAGCTTACCACACTCMAAGGACATCGCCAACGTCGCGCGA	516
Oy	180	GCAGGTATGTAGAATTCGGCTCCGAANAGATCACCAAACAACACTGTCTCAAGCTGGCAAG	239
D	515	ACAGGTGTTCCAGANTCGCTCGAAAAGTTTCAACCAACGAACACTGTGTGAACCTGGGCAA	456
Oy	240	CAGCGTGGCCGAGCTGGCCGACAGCAATGACGTGATGTGCATTCGATCACCCATGGCAC	299
D	455	GACCGTCCGCAAGCTGGCCGATAGGAGACAGGTGACGCGCATCTGTATCACCAACGATAC	396
Oy	300	CGAACACCTTGAAAGAAACCGCCTTACTTTTGAACCTCGTGAAAAAGACCAAGCCGAT	359
D	395	CGAACACCTTGAAAGAGAACCGCCTACTTCTTCACTCGTGTGAGACACACGAGAAGCTTAT	336
Oy	360	CGTGTGGTTCGGTTTCATATGCGGCCCGGACCGCCCATGTCCGCCCAACGGCATGTCTCAACT	419
D	335	CGTGTGGTTCGGTTCGATGATGCGCCCGGACCGCATGTTCGCCCAACGGCATGTCTCAACT	276
Oy	420	GTACAAACGCGTGGCCCTGGCCGACAGCAACAAGACTCGCGCGCAAGSGCGTGTGTATC	479
D	275	GTACAAACGCGCGTGGCGGTGGCCCGGACAAAGTCGGCACGCGGCAAGSGCGTGTGTATC	216
Oy	480	CATGAACGACGAGATTCAGTCCGGCGGTGACGTGACGAAGTGCATCAATCAAGACCGA	539
D	215	CATGAACGACGAGATTCCTCTCGGCGCGGACGCGAGCAAGATGTGCATCAAGACCGA	156
Oy	540	AGCCTTCAAGAGCGCTTGGGGCCCGCTTGGGCATGTGTGGAAGCAAGTGTACTGTT	599
D	155	AGCGTTCAAGAGCCCGTGGGGCCCGCTGGGCATGTGTGTGAGAGCAAGACTACTGTT	96
Oy	600	CCGCGCTGGCGG 610	
D	95	CCGCGCACCGG 85	
RESULT 2	BZ571362	871 bp DNA linear GSS 17-DEC-2002	
LOCUS	msh2_1851.x1 msh Pseudomonas aeruginosa genomic clone msh2_1851,		
DEFINITION	BZ571362	genomic survey sequence.	
ACCESSION	BZ571362		
VERSION	BZ571362.1	GI:27206423	
KEYWORDS	GSS.		
SOURCE	Pseudomonas aeruginosa		
ORGANISM	Pseudomonas aeruginosa		
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
AUTHORS	Pseudomonadaceae; Pseudomonas.		
TITLE	1 (bases 1 to 871)		
JOURNAL	Spencer,D.H., Raymond,C.K., Smith,E.B., Sims,E.B., Hastings,M.,		
COMMENT	Burns,J.T., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence Variation among multiple isolates of Pseudomonas aeruginosa library J. Bacteriol. (2002) In press		
FEATURES	Contact: Chris K. Raymond		
Source	Genome Center		
	University of Washington		
	Box 352145, Seattle, WA 98105-2145, USA		
	Tel.: 2062216954		
	Fax: 2066857244		
	Email: craymond@u.washington.edu		
	Class: shotgun.		
	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/strain="MSH"		
	/db_xref="taxon:287"		
	/clone="msh2_1851"		

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/clone_1lb="msh"
/note="Environmental isolate. Whole genomic shotgun
library."
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Best Local Similarity	77.7%	Pred. No. 26-71		
Matches 491	Conservative 0	Mismatches 134	Indels 7	Gaps 2
Qy	377	TGCGCCCCGGCACC	GATGTCGCGCCAGCGGATGCTCAACCTGTATCAACGCGCCGTGCGC	436
Db	34	TGGGTATCCGAGCC	CCCCCTCGAGGGTTCAGCGGTATCGATTAAGCTTGATATCAATTT---CC	90
Qy	437	TGGCGACACCAACA	AGACTCTCGCGCGGCAAGGGCGGTGTGTGACCATGAAAGACGATATCC	496
Db	91	TGACGCCGATMACT	CGCACGCGGCAAGGGCGGTGTGTATCACAATGACACGAGATTC	150
Qy	497	AGTCGGGCGGTGA	CGTGAAGTGCATCAACATCAAGACCGAAGCCTTCAAGAGCGCT	556
Db	151	TCTCGGCGCGGAC	CGCAGCAAGATGTGTCAATCAAGACCGAAGCGTGCAGAGCCGT	210
Qy	557	GGGGCCCCGCTGG	GGGATGTGTGGAAGGCAAGTGTATCTGTTTCCGCTGCGCGCACG	616
Db	211	GGGGCCCCGCTGG	GATGTGTGTGGAAGGCAAGTGTATCTGTTTCCGCGCACCGTGAAGC	270
Qy	617	GCCACAGGTCATC	CTCGAGTTTCGACATCAAGCAGATCAGCAGCCTGCCAGGTGACA	676
Db	271	GGCACAGGTGAAT	CTCGAGTTTGCACATCAAGCAGATCTTTCGCGCTCCGGTGGAAA	330
Qy	677	TTCGCTTACAGTAT	ATGCAAGTCAACCGACACGCGCTTCAAGGCGCTTGGCACAAACGGCG	736
Db	331	TTCGCTTACAGTAT	AGGTGAAGTCAACCGACACGCGCTTCAAGGCGCTTGGCACAAACGGCG	390
Qy	737	CCAAGGCGTATCAT	ATGCGGCAACCGGCAATATGCTCGTGTGCTCGCGGCTGTGTCAG	796
Db	391	CCAAGGCGATCAT	CAATGCGGCAACCGGCAATATGCTCGTGTGCTCGCGGCTGTGTCAG	450
Qy	797	CCTGTGAGAGCTG	CGCAAGACGGCGGTGCATCATTC---GTTGTCACTGTCAACAG	852
Db	451	CCTGTGTAGGAAT	CTGCGCAAGACGGCGGTGCATCATTTATTCGCGTCTGCGCATATGCC	510
Qy	853	GGCGGTTTCGTCG	CGGTAAACGCGGACAGCGCGGACCAAGAACGATCGTGCTGTGACC	912
Db	511	GGCGGTTTCGTCG	CGGTAAACGCGGACAGCGCGGACCAAGAACGATCGTGCTGTGACC	570
Qy	913	CACGACCTGAAAC	CCGCGAAGGCCCGCATCTCTGGCGATGTGTGCAATGACCAAGACCCAG	972
Db	571	CACGACCTGAAAC	CCGCGAAGGCCCGCATCTCTCTGGCGATGTGTGCAATGACCAAGACCCAT	630
Qy	973	GACAGCAAGAGCT	GCAGCGCATTTTCTGGGA	1004
Db	631	GACATGATGAGCT	GATCGGATTTTGGAA	662

RESULT 3

LOCUS B2570599/c

DEFINITION msh2_1446.y2 msh Pseudomonas aeruginosa genomic clone msh2_1446,

ACCESSION B2570599

VERSION B2570599.1 GI:27205660

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

ORGANISM Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 768)

Spencer,D.H., Raymond,C.K., Smith,B.E., Sims,B.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.

Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library J. Bacteriol. (2002) In press

CONTACT: Chris K. Raymond

Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: cgraymond@u.washington.edu
Class: Shotgun.

FEATURES
source
1. .802
Location/Qualifiers

/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="MSH"
/db_xref="taxon:287"
/clone="mh2_1835"
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/note="Environmental isolate. Whole genomic shotgun library."

ORIGIN

Query Match 13.7%; Score 139; DB 8; Length 802;

Best Local Similarity 71.0%; Pred.No.3.1e-19;
Matches 184; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

82 GCGGCCAAGCGGCCCACTCAACAGGCTGGCGTGCACAGCTGATTGCCGC 141
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320 GCGCCCAACGCGCCCTCCCAACCCGCCAGGTCCCGGTGACCACTGGCGGAGA 261
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142 GTGCCGAGCTGGCCGACCTGCGCAATGTGCGCGGAGAGGTGATGAGATGCCCTCC 201
|||
260 GTACCGCACTCAAGGCACTCTCATCTCCGCGGACAGAGTTCAGATGCCCTTG 201
|||
202 GAAAGCATCAACCAACGACCACTGCTCAAGCTGGCAAGAGCGTGGCCGAC 261
|||
200 GATAGCTTACCATTCAGAACTGCTGATCTGGCCAAAGCGTCAACGACCTGTCCGAT 141
|||
262 AGCATGAGCTGATGATGCTCATCAACCATGACACCGACCTTGGAAAGACCGGC 321
|||
140 AACGACGAGCTGACGCGATGTGATGCTCTCGTACGACACCGTGAAGAGACCGCC 81
|||
322 TACTTTTGAACCTCGTG 340
|||
80 TCTTCTCAACCTCGGGG 62
|||

RESULT 6
AO157105 644 bp DNA linear GSS 12-SRP-1998
LOCUS
DEFINITION
nbx0008P12r CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbx0008P12r, genomic survey
sequence.

ACCESSION
AO157105
VERSION
AO157105.1 GI:3554130
KEYWORDS
GSS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 644)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
CONTACT: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAACAGCTATGACATG
Class: BAC ends
High quality sequence stop: 424.
Location/Qualifiers

FEATURES

source

1. .644
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/mol_type="genomic DNA"
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/clone="nbx0008P12r"
/clone_1ib="msn"
/libse_type="leaf"
/lab_host="B. coli DH10B"
/clone_1ib="CUGI Rice BAC Library"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arunaganesan and Barley, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9%. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."

ORIGIN

Query Match 9.0%; Score 91.4; DB 8; Length 644;

Best Local Similarity 50.3%; Pred.No.4.2e-09;
Matches 224; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

175 GCGAGCAGGTGATGATGATGCTCCGAAAGCATCACCAAGCACTGCTCAAGCTG 234
|||
57 GTGATGATTAATTAACGCTCGGAGCTTTCATCTGCTGGAAGCCCTTGTCTTC 116
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235 GCAACAGAGGTGCGGAGCTGCGCAGCAAGATGACGTGATGATGATGATGATGAT 294
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117 GCCTGAGAGCAAGAGACATCTGCGCCAGCCCAAGATGACGAGTGTCTGACGAC 176
|||
235 GGCACCGACACCTGGAAGAAACCGCTTACTTTTGAACCTGTGGAAGAACCGACAG 354
|||
177 GGAACCGACACATGAGAGAGAGCGCTATATGAGCGCATCTTCATCATGACGAGAAG 236
|||
355 CGGATGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 414
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237 CCGTGTGATTTTACCGGATGCGGAGCGGACGATGAACCGATGATGATGATGATGATGAT 296
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415 AACCTGTACACGCGGCGCTGCGCAGCAAGATGATGATGATGATGATGATGATGATGAT 474
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297 AACATTTGCGGAGCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 356
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475 GTGACCATGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 534
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357 TTGTGTTTGAACAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 416
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535 ACCGAAGCTTGAAGAGGCGCTGCGGCGGCTGAGGATGATGATGATGATGATGATGATGAT 594
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417 ACCGACAGCTTATTTTCTGCGAATGAGGAACTGGTGAAGTGAATGATGATGATGATGAT 476
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595 TGGTTCCGCTGCGGCGCAAGCGCC 619
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477 ATCGTGACCGCGCGCGGTGCGC 501
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RESULT 7
BH376509/c 757 bp DNA linear GSS 10-DEC-2001
LOCUS
DEFINITION
AG-ND-137P15.TF.1 ND-TAM Anopheles gambiae genomic clone
AG-ND-137P15, genomic survey sequence.
ACCESSION
BH376509

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VERSION      BH376509.1  GI:17322651
KEYWORDS
SOURCE
ORGANISM      Anopheles gambiae (African malaria mosquito)
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
               Anopheles.
REFERENCE
  1 (bases 1 to 757)
    Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
    Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
    Gardner, M.J. and Collins, F.H.
    Construction of a BAC library and generation of BAC end
    sequence-tagged connectors for genome sequencing of the African
    malaria mosquito Anopheles gambiae
    Mol. Genet. Genomics 268 (6), 720-728 (2003)
JOURNAL
MEDLINE
PUBMED
  12655398
COMMENT
  Other GSSs: AG-ND-137P15.TR.1
  Contact: Brendan J Loftus
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0208
  Fax: 301 838 3543
  Email: b.loftus@igr.org
  This clone is from an A. gambiae BAC library (ND-TAM) provided by
  F.H. Collins and sequenced by The Institute for Genomic Research
  (TIGR). The BAC library was generated from A. gambiae PEST strain
  DNA. All DNA was extracted from newly hatched first instar larvae
  to minimize the inclusion of DNA from microorganisms that inhabit
  the gut. The DNA is derived from mixed sexes of larvae. The BAC
  library was constructed at Texas A&M University BAC Center
  University, College Station, Texas 77843-2123, USA using a HindIII
  partial digest.
  Seq primer: M13 For
  Class: BAC ends.
FEATURES
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ORIGIN
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  Best Local Similarity 50.6%; Pred. No. 9.3e-09;
  Matches 217; Conservative 0; Mismatches 212; Indels 0; Gaps 0;
  121 GTCGACACGCTGATTCGCGCGCTGCGGAGCTGGCGACCTGGCCAATGTGCGCGGAG 180
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  Qy      181 CAGGTGATGCAATCGCTCCGAAAGCATCACAAGAGAGACTGCTCAAGCTGGGAAAC 240
  Db      570 AACTTATCCAAAGCTTCATCGACTACATGAGGGCGCTGAGCGCTGCAGCTCATGTCT 511
  Qy      241 AGCGTGGCCGAGCTGGCGCAGACGATGATGATGATGATGATGATGATGATGATGATGAT 300
  Db      510 GCTGTGCAAGAGCGCTATCAACAGTCAAGAGCTGTGCGGTGATCTTTCTCATGCAAA 451
  Qy      301 GACACCTGGAAGAAACCGCTACTTTTGAACCTGTGGAAGAAAGACGACAGCCGATC 360
  Db      450 GATACGCTGAGAGAAACAGCTTTTGGCTTGATCTGACAGTGAAGTCAATAAACCAATC 391
  Qy      361 GTCTGTGATGCTTCATGAGCGCGCGCAGCGCATGTCCGCGAGCGCATGCTCAACCTG 420
  Db      390 GTCTGTGATGCTTCATGAGCGCGCGCAGCGCATGCTTCAGATCTTGAACGCTCCGCGCACTTG 331
  Qy      421 TACAAGCGCTGGCGCTGCGCAGCAACAGACTCGCGCGGCAAGGGCGCTGTGTGACC 480

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Db      330 CTTAAGCTGTGCGCATCGCTGTGATCCCAATCCAAAGATGTGCGCGCATGTGCGG 271
Qy      481 ATGAACGAGAGATTCAGTCCGCGCTGACGTGAGAGAAATTCATCAATCAAGACCGAA 540
Db      270 ATGAACGAGAGATTCAGTCCGCGCTGACGTGAGAGAAATTCATCAATCAAGACCGAA 211
Qy      541 GCCTTCAG 549
Db      210 ACTTTTAC 202
RESULT 8
BH371112/c
LOCUS
DEFINITION
  BH371112 663 bp DNA linear GSS 10-DEC-2001
  AG-ND-137P15.TR ND-TAM Anopheles gambiae genomic clone
  AG-ND-137P15, genomic survey sequence.
ACCESSION
  BH371112
VERSION
  BH371112.1 GI:17317237
KEYWORDS
SOURCE
ORGANISM      Anopheles gambiae (African malaria mosquito)
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
               Anopheles.
REFERENCE
  1 (bases 1 to 663)
    Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
    Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
    Gardner, M.J. and Collins, F.H.
    Construction of a BAC library and generation of BAC end
    sequence-tagged connectors for genome sequencing of the African
    malaria mosquito Anopheles gambiae
    Mol. Genet. Genomics 268 (6), 720-728 (2003)
JOURNAL
MEDLINE
PUBMED
  12655398
COMMENT
  Other GSSs: AG-ND-137P15.TR
  Contact: Brendan J Loftus
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0208
  Fax: 301 838 3543
  Email: b.loftus@igr.org
  This clone is from an A. gambiae BAC library (ND-TAM) provided by
  F.H. Collins and sequenced by The Institute for Genomic Research
  (TIGR). The BAC library was generated from A. gambiae PEST strain
  DNA. All DNA was extracted from newly hatched first instar larvae
  to minimize the inclusion of DNA from microorganisms that inhabit
  the gut. The DNA is derived from mixed sexes of larvae. The BAC
  library was constructed at Texas A&M University BAC Center
  University, College Station, Texas 77843-2123, USA using a HindIII
  partial digest.
  Seq primer: M13 For
  Class: BAC ends.
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    /mol_type="genomic DNA"
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    /note="Vector: pCBAC1; Site_1: HindIII"
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  Best Local Similarity 49.7%; Pred. No. 1.4e-07;
  Matches 215; Conservative 0; Mismatches 218; Indels 0; Gaps 0;
  134 TTGCGGCGTGGCGGAGCTGGCCGACCTGGCCAATGTGCGCGCGCAGCAGGTGACAGA 193
  Db      618 TTGCGTACCGTGTCTGTGTGAGCAAGTACGCCAAGATCCAGGTAAACAATTATCCAAAG 559
  Qy      194 TGCGTCCGAAAGCATCAACAGAGACTGTCTCAAGCTGGCAAGCAGCTGGCCGAGC 253

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/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PU601794"
/dev_stage="primary phase variant"
/clone_1ib="Photocladus luminescens strain W14 M13 library"
/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

ORIGIN

Query Match 8.1%; Score 82; DB 8; Length 724;
Best Local Similarity 55.1%; Pred. No. 4.2e-07;
Matches 207; Conservative 0; Mismatches 160; Indels 9; Gaps 2;

QY 44 TGGCCACCGGCGGACCATGCGGCGCTGGCGCCAGCGGCGCAACGCGCACTACC 103
DB 379 TGGCGACGGGGGAGCATATGCGGG--TGGCGGAAATCTGCATTCATCAATTAATG 323
QY 104 AGGCTGCCAAGTTGGGTGCAACAAGCTATGCGGCGGCGGAGCTGGCGGACCTGG 163
DB 322 TTCTGGAAGGGTTGCTATTGAAATTAATGCTCAATGCTGTTCTTGAGATCAAAATATCG 263
QY 164 CCAATGTGCGCGCGAGCAGTGTATGCAATCGCTCCGAAAGCATCAACAGAGAGCC 223
DB 262 CCAACTAAAGGTGAGCAGGTAGTTAGTATGTTGCGAGATATGAATGATCAAGTGT 203
QY 224 TGTCTCAAGTGGCAAGCAGGTGGCGGAGCTGGCGGCAAGATGACGTGATGATCG 283
DB 202 GGTTCAGCGTACGGAAGAAATCAAC-----GCTGATGTGCAAAACCGATGTTTG 149
QY 284 TCATCAACCATGGACCGACACCTGGAAAGAACCGCTACTTTTGAACCTGTGGAA 343
DB 148 TTTATCCCAACGGTATCTGACACATGAGAAACCGTTTACTTCTGATCTCACTAAC 89
QY 344 AGACCGCAAGCCGATGTCGTGTCGTTTCATGCGCCCGGCGGCGGCGGATGCGCG 403
DB 88 ACTGCCAAGAGCGGATGATGATGTTGGCGGATGCGGCGCATCTACGCGCTGTGCGG 29
QY 404 ACGGCAATGCTCAACT 419
DB 28 ATGGCCCGTTAAATCT 13

RESULT 11
AQ500605/c 766 bp DNA linear GSS 29-APR-1999
LOCUS V36C6 mtn-3xHA/lacZ insertion library Saccharomyces cerevisiae
DEFINITION genomic 5', genomic survey sequence.
ACCESSION AQ500605.1 GI:4706315
VERSION GSS.
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetiales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 766)
Rosa-Macdonald, P., Roemer, T., Coelho, P. S. R., Agarwal, S., Kumar, A.,
desBergues, S. A., Cheung, K.-H., Sheehan, A., Symoniatidis, D., Jansen, R.,
Umanaky, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lungo, R.,
Hager, K., Miller, P., Roeder, G. S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
JOURNAL CONTACT: Kumar A
COMMENT Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumaryale.yale.edu
te of mtn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTCTTGGAAATGAC

FEATURES Class: transposon-tagged.
Location/Qualifiers
source 1..766
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/lab_host="S. coli"
/clone_1ib="mtm-3xHA/lacZ insertion library"
/note="Vector: pHS6-Sal; A yeast genomic DNA library
(lacking mitochondrial DNA) was prepared in pHS6-Sal;
genomic DNA was size-fractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
subsequently mutagenized with a mtn-3xHA/lacZ
mitransposon containing lacZ, URA3, and tet resistance."

ORIGIN

Query Match 8.0%; Score 81; DB 8; Length 766;
Best Local Similarity 50.6%; Pred. No. 6.9e-07;
Matches 195; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 120 CGTGCAAGCTATTTGCGGCGTGGCGGAGCTGGCGGACCTGCGCAATGTGCGCGCA 179
DB 534 CGTATATGATTTAATGAAAGCCGTCATCTTAAGCTGGAAGGAGATCTGACTATCT 475
QY 180 GCAGTATGATGATGCGCTCCGAAAGCATCAACAGACAGACTGCTCAAGCTGGCAAG 239
DB 474 TCAAGTGTCTAAGCTTGTTCACATTTCTTAACATTAAGCATCTATCCATTTATCA 415
QY 240 CAGCGTGGCGAGCTGGCGGACAGCAATGACGTGATGCGATGTCATGACCCAGGAC 299
DB 414 CGGTATCTCGAGGCACTAGCTGTGATGATTAACGTGATGCGGTGTGCACTATGAGAC 355
QY 300 CCAACACCTGGAAGAAACCGCTTATTTTGAACCTGTGGAAGAAACCGCAAGCCGAT 359
DB 354 CCACTATGAGAGAAACAGCTTTCTTGAATTTGACATTAATTCAGAAAGCAGT 295
QY 360 CGTGTGTGTCGTTCATGCGCGCGGCAACGCGGATGTCGCGGAGGATGCTCAACT 419
DB 294 ATGTATCGAGGCGCTATGCTGTCACGCTGCGGATGTCGCTGATGCGGCGGATGTT 225
QY 420 GTTCAAGCGCGTGGCGGCGGCAAGCAAGACTGCGCGGCGGAGGCGTGTGTGAC 479
DB 234 ATATCAAGCAGGTCTATGCTGCTTCTGGAATCACTGCGGTGCGGAGATGATCAC 175
QY 480 CATGAACGACGATCACTCGGG 504
DB 174 TCTTAACGATCGTATGCTCTGGG 150

RESULT 12
AQ500657/c 843 bp DNA linear GSS 29-APR-1999
LOCUS V34F11 mtn-3xHA/lacZ insertion library Saccharomyces cerevisiae
DEFINITION genomic 5', genomic survey sequence.
ACCESSION AQ500657.1 GI:4706367
VERSION GSS.
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetiales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1 (bases 1 to 843)
Rosa-Macdonald, P., Roemer, T., Coelho, P. S. R., Agarwal, S., Kumar, A.,
desBergues, S. A., Cheung, K.-H., Sheehan, A., Symoniatidis, D., Jansen, R.,
Umanaky, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lungo, R.,
Hager, K., Miller, P., Roeder, G. S. and Snyder, M.
Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Gene Disruption
Unpublished (1999)
JOURNAL CONTACT: Kumar A
COMMENT Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA

Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 te of mtn-3xHA/lacZ insertion.
 Seg primer: GGCTTCTTCTTGGAAGTAC
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES

source

1. 843
 /organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /db_xref="taxon:4932"
 /lab_host="E. coli"
 /clone_1lb="mtn-3xHA/lacZ insertion library"
 /note="Vector: pHS86-Sal; A yeast genomic DNA library
 (lacking mitochondrial DNA) was prepared in pHS86-Sal;
 genomic DNA was size-fractionated (DNA of roughly 2-3 kb
 in length) prior to cloning. This library was
 subsequently mutagenized with a mtn-3xHA/lacZ
 minitransposon containing lacZ, URA3, and tet resistance."

ORIGIN

Query Match 7.8%; Score 78.6; DB 8; Length 843;
 Best Local Similarity 49.9%; Pred. No. 2.3e-06;
 Matches 192; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 120 CGTCGACAGCTGATTCGCGCGCGGAGCTGCGGACCTGCGCAATGTGCGCGCA 179
 DB 671 CGTAATGATNTATAGAGCCCTCCATCTTTAGCTGAGAGGACATCTGACTATCT 612
 QY 180 GCAGTGATGCAATGCTCTCGAAGACATCAACGACGACTGCTCAAGTGGCAAG 239
 DB 611 TCAAGTGTCAACGTTGTTCAATCTTANACTATAGCACTGATCCCATTTATCA 552
 QY 240 CAGCGTGGCGGAGCTGCGGACGACATACGTCGATGATGATGATGATGATGATGAT 299
 DB 551 CGGTATCTCGAGGCACTAGCTTCTGATGATGATGATGATGATGATGATGATGAT 492
 QY 300 CGACACCTGAGAGAAACGCTACTTTTGAACCTCTGAGAAAGACGACGACGACGAT 359
 DB 491 CGACATATAGAGAGAGACAGCTTTCTTTAGATTGACATTAATTGAGAGAGCAAT 432
 QY 360 CGTGTGTTGCTTCATGCGCGCGGACGCGGACGATGTCGCGGACGATGCTCACT 419
 DB 431 ATGTATCGAGGCGCTATGCTGCTCAAGCACTGCTGCTGATGCGCCATGATTTT 372
 QY 420 GTTCAAGCGCGTGGCGCGGCGGACGACGATGCTGCGGCGGCGGCGTGTGATGAC 479
 DB 371 ATATCAAGCAGTGTATGCTGCTTCTGAGAAATCACTGGGTCGTGGCAAGATGATC 312
 QY 480 CATGAACGACGAGATCCAGTCCGGG 504
 DB 311 TCTAAAGATCGATTGCTCTGGG 287

RESULT 13
 AOS01722/c 453 bp DNA linear GSS 29-APR-1999
 LOCUS V15G1 mtn-3xHA/lacZ Insertion library Saccharomyces cerevisiae
 DEFINITION genomic 5', genomic survey sequence.
 ACCESSION AOS01722
 VERSION AOS01722.1 GI:4707372
 KEYWORDS GSS.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 1 (bases 1 to 453)
 Rose-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
 deBragas, S.A., Cheung, K.-H., Sheehan, A., Symonakis, D., Jansen, R.,
 Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
 Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
 Gene Disruption

JOURNAL

Unpublished (1999)
 Contact: Kumar A

COMMENT

Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
 Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 te of mtn-3xHA/lacZ insertion.
 Seg primer: GGCTTCTTCTTGGAAGTAC
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES

source

1. 453
 /organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /db_xref="taxon:4932"
 /lab_host="E. coli"
 /clone_1lb="mtn-3xHA/lacZ insertion library"
 /note="Vector: pHS86-Sal; A yeast genomic DNA library
 (lacking mitochondrial DNA) was prepared in pHS86-Sal;
 genomic DNA was size-fractionated (DNA of roughly 2-3 kb
 in length) prior to cloning. This library was
 subsequently mutagenized with a mtn-3xHA/lacZ
 minitransposon containing lacZ, URA3, and tet resistance."

ORIGIN

Query Match 7.3%; Score 73.6; DB 8; Length 453;
 Best Local Similarity 52.6%; Pred. No. 2.5e-05;
 Matches 160; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 248 CCGAGCTGGCCGACGACATAGCTGATGATGATGATGATGATGATGATGATGAT 307
 DB 366 CCGAGGCACTAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 307
 QY 308 TGGAGAAACCGCCCTACTTTTGAACCTCTGAGAAAGACGACGACGATGCTGTG 367
 DB 306 TGGAGAGACAGCTTCTTCTTGAATTGACATTAATTGAGAGAGGACGATGATG 247
 QY 368 TCGTTCATGCGCGCGGACGCGGACATGTCGCGGACGCGGATGCTCACTGTAAC 427
 DB 246 CAGCGGCTATGCTGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
 QY 428 CCGTGGCCGTGGCCAGCAAGAACTGCGCGGCGGAGGCGTCTGCTGACATGAA 487
 DB 186 CAGTGTCTATGCTGCTCTTCTGAGAAATCACTGCGTCTGCGGACGATGATCTTAA 127
 QY 488 ACGAGATCCAGTCCGCGGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 547
 DB 126 ATGTAATGCTCTGCGGTTTGGACACGAAATGATGCAACTCTTTAGTATCA 67
 QY 548 AGAG 551
 DB 66 GGGG 63

RESULT 14
 AOS01723/c 459 bp DNA linear GSS 29-APR-1999
 LOCUS V15G2 mtn-3xHA/lacZ Insertion library Saccharomyces cerevisiae
 DEFINITION genomic 5', genomic survey sequence.
 ACCESSION AOS01723
 VERSION AOS01723.1 GI:4707373
 KEYWORDS GSS.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 1 (bases 1 to 459)
 Rose-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,
 deBragas, S.A., Cheung, K.-H., Sheehan, A., Symonakis, D., Jansen, R.,
 Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R.,
 Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
 Gene Disruption

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 21:13:22 ; Search time 168 Seconds
(without alignments)
773.521 Million cell updates/sec

Title: US-09-842-628-2

Perfect score: 1680

Sequence: 1 KEVENQQLKAVVILATGST.....MVAMTKQDSKEQLGRIFWEY 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19806:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20038:*\n8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1680	100.0	336	2	AAR59739 Pseudomon
2	1432.5	85.3	393	7	ABO73618 Pseudomon
3	1063.5	63.3	374	6	ADA35175 Actinobac
4	782	46.5	348	3	AAW90867 L-asparag
5	758	45.1	375	8	AD136574 Bacillus
6	749	44.6	327	2	AAR21555 L-asparag
7	749	44.6	348	1	AAW70348 Sequence
8	749	44.6	348	6	ABP98617 Erwinta C
9	717	42.7	364	2	AAW98609 H. pylori
10	711	42.3	356	7	ABO61384 Klebsiell
11	710.5	42.3	346	7	ADP05106 Bacteri
12	685.5	40.8	348	6	ABM68938 Photoc
13	677.5	40.3	326	6	ABP98616 Mature B
14	677.5	40.3	348	6	ABP98615 Erwinta C
15	602.5	35.9	378	8	ADDO07179 Aspergill
16	560.5	33.4	378	8	ADDO07181 Aspergill
17	559	33.3	374	8	ADDO07183 Aspergill
18	536.5	31.9	378	8	ADN97130 ASPA01 as
19	535.5	31.9	451	8	ADDO07187 Fusarium
20	528	31.4	371	8	ADDO07185 Fusarium
21	517	30.8	379	8	ADDO07189 Penicill
22	485	28.9	362	8	ADDO07190 Saccharom
23	465	27.7	100	2	AAK37660 Pseudomon
24	372.5	22.2	333	7	ADH86728 Enterococ
25	361.5	21.5	322	4	AAK82409 S. epider

26	361.5	21.5	326	5	ABP38389 Staphyloc
27	360.5	21.5	323	5	ABBS4049 Lactococc
28	356	21.2	320	6	ABU02502 S. pneumo
29	356	21.2	320	8	ADK47071 Streptoco
30	356	21.2	320	8	ADM92242 S pneumon
31	356	21.2	321	8	ADR94759 Novel S.
32	349.5	20.8	322	6	ABM70762 Streptoco
33	332	19.8	321	5	ABP27237 Streptoco
34	331.5	19.0	324	7	ADC95330 R. faeciu
35	318.5	19.0	320	5	ABP27236 Streptoco
36	317	18.9	320	5	ABP49122 Listeria
37	300	17.9	297	5	ABP30464 Streptoco
38	294.5	17.5	114	5	ABU51451 Helicobac
39	291	17.3	450	8	ADN46622 Thermococ
40	279	16.6	439	4	AAK96655 Putative
41	269.5	16.0	458	7	ADM26993 Hyperther
42	251	14.9	325	4	AAK79696 Corynebact
43	251	14.9	325	4	AAK92092 C glutamyl
44	226.5	13.5	340	4	AAK96780 Putative
45	216.5	12.9	328	8	ADN46369 Thermococ

ALIGNMENTS

RESULT 1
AAR59739
ID AAR59739 standard; protein; 336 AA.
XX
AC AAR59739;
XX
DT 25-MAR-2003 (revised)
DT 12-JUN-1995 (first entry)
XX
DE Pseudomonas glutaminase.
XX
KM Glutaminase; antiviral; virucide; anticancer; cancer therapy; HIV virus;
KM Gene therapy; Escherichia coli.
XX
OS Pseudomonas sp.
XX
PN WO9413817-A1.
XX
PD 23-JUN-1994.
XX
PF 04-DEC-1992; 92WC-US010421.
XX
PR 04-DEC-1992; 92WC-US010421.
XX
PA (MEME-) MB MEDICAL ENZYMES AG.
XX
PI Roberts J, Macallister TW, Sethuraman N, Freeman AG;
XX
XX WPI; 1994-217891/26.
XX
DR N-PSDB; AAK68438.
XX
PT Recombinant glutaminase derived from Pseudomonas 7A - expressed in E.
PT coli to increase yield and avoid Pseudomonas endotoxins for antiviral and
PT anticancer therapy.
XX
PS Disclosure; Page 33-34; 60pp; English.
XX
PS Chromosomal DNA from Pseudomonas sp. 7A (ATCC 29598) was used to
CC construct a genomic library in Escherichia coli DE392. Screening with
CC mixed oligonucleotide probes was used to isolate a glutaminase- encoding
CC clone. This was sequenced using the primers given in AAK68439-47. The
CC gene can be used to manufacture recombinant glutaminase, free of
CC Pseudomonas exotoxin, for use in e.g. HIV and cancer therapy. The gene
CC may also be used in gene therapy protocols. (Updated on 25-Mar-2003 to
CC correct PN field.)
XX
SQ Sequence 336 AA;

Query Match 100.0%; Score 1680; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 5.7e-131;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVENOQKLANVILATGTTAGAGASANSATYQAAGVYDKLAGVPELADLANVGE 60
 DB 1 KEVENOQKLANVILATGTTAGAGASANSATYQAAGVYDKLAGVPELADLANVGE 60
 QY 61 QVMOJASESITNDLLKLASSVAELADSDVDGIVITHTGDTLBEETAYFLNVEKTDKPI 120
 DB 61 QVMOJASESITNDLLKLASSVAELADSDVDGIVITHTGDTLBEETAYFLNVEKTDKPI 120
 QY 121 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 180
 DB 121 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 180
 QY 181 AFKSMGPIGMVBEKSYWFRLPARKHTVNSFPDIKQISLPQVDIAYSIGNVTDTAYKA 240
 DB 181 AFKSMGPIGMVBEKSYWFRLPARKHTVNSFPDIKQISLPQVDIAYSIGNVTDTAYKA 240
 QY 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSRQGGFVLRNAEQPDDKND 300
 DB 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSRQGGFVLRNAEQPDDKND 300
 QY 301 WVVAHDLPQKARILAMVAMTKTQDSKEIQRIFFWEY 336
 DB 301 WVVAHDLPQKARILAMVAMTKTQDSKEIQRIFFWEY 336

RESULT 2

ABO73618
 ID ABO73618 standard; protein; 393 AA.

XX AC ABO73618;

XX DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #5793.

XX KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfeld MJ, Nolling J, DeLoughery C, Bush D;

XX WI MPI; 2003-615309/58.

XX DR N-PsDB; ABD07189.

XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 useful as molecular targets for diagnostics, prophylaxis and treatment of
 pathological conditions resulting from bacterial infection.

XX PS Dielcousey; SEQ ID NO 22364; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant

CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 393 AA;

Query Match 85.3%; Score 1432.5; DB 7; Length 393;
 Best Local Similarity 84.3%; Pred. No. 2.6e-110;
 Matches 284; Conservative 22; Mismatches 30; Indels 1; Gaps 1;

QY 1 KEVENOQKLANVILATGTTAGAGASANSATYQAAGVYDKLAGVPELADLANVGE 60
 DB 57 KEVENOQKLANVILATGTTAGAGASANSATYQAAGVYDKLAGVPELADLANVGE 116
 QY 61 QVMOJASESITNDLLKLASSVAELADSDVDGIVITHTGDTLBEETAYFLNVEKTDKPI 120
 DB 117 QVMOJASESITNDLLKLASSVAELADSDVDGIVITHTGDTLBEETAYFLNVEKTDKPI 176
 QY 121 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 180
 DB 121 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 180
 QY 177 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 236
 DB 177 VVGSNRPETAMSADGMLNLYNAVAASNDKSRGKGVLTVMNDEIQSGRDVSKSINIKTE 236
 QY 181 AFKSMGPIGMVBEKSYWFRLPARKHTVNSFPDIKQISLPQVDIAYSIGNVTDTAYKA 240
 DB 237 AFKSMGPIGMVBEKSYWFRLPARKHTVNSFPDIKQISLPQVDIAYSIGNVTDTAYKA 296
 QY 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSRQGGFVLRNAEQPDDKND 299
 DB 297 LAQNGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSRQGGFVLRNAEQPDDKND 356
 QY 300 DMVVAHDLPQKARILAMVAMTKTQDSKEIQRIFFWEY 336
 DB 357 DMVVAHDLPQKARILAMVAMTKTQDSKEIQRIFFWEY 393

RESULT 3

ADA35175
 ID ADA35175 standard; protein; 374 AA.

XX AC ADA35175;

XX DT 20-NOV-2003 (first entry)

XX DE Acinetobacter baumannii protein #2336.

XX KM Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
 plant biocontrol agent.

XX OS Acinetobacter baumannii.

XX PN US6562958-B1.

XX PD 13-MAY-2003.

XX PF 04-JUN-1999; 99US-00328352.

XX PR 09-JUN-1998; 98US-0088701P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Breton G, Bush D;

XX WI MPI; 2003-576092/54.

XX DR N-PsDB; ADA31049.

XX PT New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
 for diagnosing a bacterial disease, as components of antibacterial
 vaccines, as targets for antibacterial drugs, or as biocontrol agents for

PT plants.

XX Example; SEQ ID NO 6462; 328bp; English.

CC The invention relates to isolated *Acinetobacter baumannii* nucleic acids.
 CC The *A. baumannii* nucleic acids and polypeptides are useful as reagents
 CC for diagnosing a bacterial disease, as components of antibacterial
 CC vaccines, as targets for antibacterial drugs, to detect the presence of
 CC *A. baumannii* and other *Acinetobacter* species in a sample, in screening
 CC compounds for the ability to interfere with the *A. baumannii* life cycle
 CC or to inhibit *A. baumannii* infection, and as biocontrol agents for
 CC plants. The present sequence represents the amino acid sequence of an *A.*
 CC *baumanni* protein.

XX Sequence 374 AA;

Query Match 63.3%; Score 1063.5; DB 6; Length 374;
 Best Local Similarity 64.7%; Pred. No. 1.1e-79;
 Matches 213; Conservative 45; Mismatches 68; Indels 3; Gaps 2;

QY 11 NVVILATGTTAGAGSAAASATYQAAGVNDKLIAGVPELADLANVREGQVMQIASSEI 70
 DB 46 NVVVAATGTTIAGAGSAAASATYTAAPVDALINAVPQIDLANVSGIQALQVASSSEI 105
 QY 71 TNDDELKLASSVAELADSDVDGIVITHTGDTLEETAYFLNVEKTDKPIVVGSMRPET 130
 DB 106 TDKEILQIARQVNELVKERTVAGVITHTGDTLEETAYFLNVEKTDKPIVVGSMRPET 165
 QY 131 AMSADGMLNLVNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFKSAWPIG 190
 DB 166 ALSADGPIPLVSAVALAASDANKKGMVLMNDSIPARDVTGGINIHNAFVSGWALG 225
 QY 191 MYVEGKSVYFRLPAKHTYNSSEFDIKQI--SLPQVDIAYSIGNVDTAYKALAQNGAK 248
 DB 226 TLVEGKPYFROSVKHTYNSSEFDIKQI--SLPQVDIAYSIGNVDTAYKALAQNGAK 285
 QY 249 LIHAGTNGSVSRVVPALQELR-KNGVOIIRSSRQGGFVLRNAEOPDDKNDWVAHDL 307
 DB 266 ITHAGTNGSVAKYIVPTQNLHDKNGIQIIRSSRVPQGFVLRNAEOPDDKNDWVAHDL 345
 QY 308 NPQAKRIILAMVAMTKQDSKELQRIFWEX 336
 DB 346 NPQAKRIILALALTKTNDANKIQRMFWQY 374

RESULT 4
 AAM90867
 ID AAM90867 standard; protein; 348 AA.

AC AAM90867;
 XX 30-JUN-2000 (first entry)
 DT 30-JUN-2000 (first entry)
 XX L-asparaginase protein.
 DE L-asparaginase protein.
 XX L-asparaginase; fermentation; 89.
 KM Unidentified.
 OS Unidentified.
 XX CN1237633-A.
 PN CN1237633-A.
 XX 08-DEC-1999.
 PD 08-DEC-1999.
 XX 01-JUN-1999; 98CN-00102046.
 PF 01-JUN-1999; 98CN-00102046.
 XX 01-JUN-1999; 98CN-00102046.
 PR 01-JUN-1999; 98CN-00102046.
 XX (MICK-) INST MICROBIOLOGY CHINESE ACAD SCI.
 PA Qian B, Wang Y, Meng G;
 XX WPI; 2000-351194/31.
 XX N-PSDB; AAX62634.
 DR

XX New structured L-asparaginase bacterial host cell and its production
 PT culture.

XX Dislosure; Fig 2; 12pp; Chinese.

PS This invention describes a novel L-asparaginase-producing recombinant
 CC bacteria and its fermentation culture method. The new cell is produced
 CC using standard recombinant techniques. The enzyme gene expressed in the
 CC cell is different from the reported enzyme gene in sequence, and its
 CC individual amino acid composition is also different. The culture medium
 CC adopted for culturing the new bacterial cells is cheap and easily
 CC available, and the fermentation process used to grow the cells and
 CC express the enzyme is simple and easy to implement. This sequence
 CC represents an L-asparaginase which is described in the method of the
 CC invention

XX Sequence 348 AA;

Query Match 46.5%; Score 782; DB 3; Length 348;
 Best Local Similarity 48.3%; Pred. No. 2.3e-56;
 Matches 159; Conservative 59; Mismatches 107; Indels 4; Gaps 3;

QY 9 LANVILATGTTIAGAGSAAASATYQAAGVNDKLIAGVPELADLANVREGQVMQIASSEI 68
 DB 23 LENITILATGTTIAGAGSAAASATYTAAPVDALINAVPQIDLANVSGIQALQVASSSEI 81
 QY 69 SITNDDELKLASSVAELADSDVDGIVITHTGDTLEETAYFLNVEKTDKPIVVGSMRPET 128
 DB 82 DNDVDVLLAKKIN--TDCDCTIDGPFVITHTGDTLEETAYFLNVEKTDKPIVVGSMRPET 139
 QY 129 GTAMSADGMLNLVNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFKSAWPIG 187
 DB 140 STMSADGPFNLVNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFKSAWPIG 199
 QY 188 PLGMYVEGKSVYFRLPAKHTYNSSEFDIKQI--SLPQVDIAYSIGNVDTAYKALAQNGAK 247
 DB 200 PLGYIHNGKIDYQRIIPARKHTSDTPEVSKNELPKVGIIVNVAASDLPALALVDAGVD 259
 QY 248 ALIHAGTNGSVSRVVPALQELR-KNGVOIIRSSRQGGFVLRNAEOPDDKNDWVAHDL 307
 DB 260 GIVSGVGVNGNLKYSVFTPLTAARKNGTAVVSSVPTGATTQDAEVDPAKGFVAASGTL 319
 QY 308 NPQAKRIILAMVAMTKQDSKELQRIFWEX 336
 DB 320 NPQAKRIILQALALTKTNDANKIQRIFWQY 348

RESULT 5
 ADI36574
 ID ADI36574 standard; protein; 375 AA.

AC ADI36574;
 XX 15-APR-2004 (first entry)
 DT 15-APR-2004 (first entry)
 XX Bacillus subtilis L-asparaginase protein.
 DE Bacillus subtilis L-asparaginase protein.
 XX Secreted protein; L-asparaginase; acute lymphocytic leukemia; therapy;
 KM enzyme.
 XX Bacillus subtilis.
 OS Bacillus subtilis.
 XX Key Location/Qualifiers
 FH Peptide 1..23
 FT /label=Signal_peptide
 FT Protein 24..375
 FT /note="Mature Bacillus subtilis L-asparaginase protein"
 XX US2003186380-A1.
 XX 02-OCT-2003.
 XX

PF 01-APR-2003; 2003US-00406025.
 XX
 PR 01-APR-2002; 2002US-0369192P.
 XX
 XX (NOVO) NOVOZYMES BIOTECH INC.
 PA Thomas MD, Sloma A;
 XX
 PI
 XX WPI; 2004-088916/09.
 DR N-PSDB; ADI36573.
 XX
 PT Production of a secreted polypeptide having L-asparaginase activity for
 PT treating leukemia, comprises cultivating a host cell comprising a nucleic
 PT acid having a sequence encoding a secretory signal peptide linked to a
 PT second sequence.
 PS
 XX Claim 34; SEQ ID NO 2; 22pp; English.
 XX
 CC The present invention relates to recombinant methods for producing
 CC secreted polypeptides having L-asparaginase activity. The invention is
 CC useful for production of a secreted protein having L-asparaginase
 CC activity, for use in producing L-asparagine from L-asparagine. The
 CC invention is useful for treatment of leukemia such as acute lymphocytic
 CC leukemia. The present sequence is the Bacillus subtilis L-asparaginase
 CC protein.

XX Sequence 375 AA;

Query Match 45.1%; Score 758; DB 8; Length 375;

Best Local Similarity 47.6%; Pred. No. 2.5e-54;
 Matches 158; Conservative 58; Mismatches 112; Indels 4; Gaps 3;

QY 6 QOKLNVLLATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADLANVREGVQMGI 65
 DB 47 KXDLPIRILATGTTAGADQSTETKAGVGVESLIBAVPEKDIANVSGEIVNV 106
 QY 66 ASESITNDLLKLASSVAELADSDVDGIVITHTDTLEETAYFLNVEKTKPIVVGVS 125
 DB 107 GSTINDKLLKLAKRINHLLASDDVDGIVITHTDTLEETAYFLNVEKTKPIVVGVS 166
 QY 126 KSPGTASADGMLNLYNAVAASNKDSRGKGLVTMNDIEIOGRDVSISINIKTEAFKS- 184
 DB 167 MPPSTLISADGSPNLNAYKAGAPAKGKGTLLVINDRIASARYVTNTTTTDFKSE 226
 QY 185 AWGPIGVVSGKSYWFRLLPAKHTVNSRPDIKQISLPQVDIAYSGVNTDTAYKALQN 244
 DB 227 EMGFPGTINAD-DIYFNNEITRKHTKOTDPSVNLDELPOVDIIYQNDGSLFLPDAVKA 285
 QY 245 GAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSRQGGFVLRNAEQPDDKNDWVVA 304
 DB 286 GAKGIYFAGSGGSLSDAAKGAADSAVKKGVTVVSTRGTNGVVTPEMDYAR--KDLAS 343
 QY 305 HDLNPOKARILAVAMTKTQDSKELORIFWY 336
 DB 344 NSLNPOKARILMLALTKTNDPOKIOAYFNEY 375

RESULT 6
 AAR21555

ID AAR21555 standard; protein, 327 AA.

XX AAR21555;

XX 10-JUN-1992 (first entry)

XX L-asparaginase.

XX Purification process; super-expression; lymphoblastic leukaemia.

XX Erwinia chrysanthemi.

XX WO9202616-A.

PD 20-FEB-1992.
 XX
 PF 02-AUG-1990; 90GB-00017002.
 XX
 PR 02-AUG-1990; 90GB-00017002.
 XX
 XX (PUBL-) PUBLIC HEALTH LAB S.
 PA
 XX
 PI
 XX Goward C;
 XX
 DR WPI; 1992-080071/10.
 XX
 PT Purificn. of Erwinia L-asparaginase - by contact with a solid medium
 PT having cation exchange groups, pref. sulphamate.
 PS
 XX Disclosure; Fig 1; 17pp; English.

CC The protein sequence was obt. from a 12 hr. seed culture of E.
 CC chrysanthemi added to a medium contg. yeast extract and Na glutamate.
 CC After centrifugation the pH was adjusted and the supernatant further
 CC centrifuged to remove any deposit. The extract was purified by a S-
 CC Sepharose Fast Flow column, having cation exchange spe. (comprising
 CC sulphamate spe.) to absorb asparaginase on the support. A degree of
 CC purificn. resulting in a specific activity >600U/mg was achieved after 6
 CC purificn. steps with a yield of 40 percent. L-asparaginase can be
 CC produced of a very high quality from an amplified process which allows
 CC for increased automation. E. chrysanthemi is known to be effective
 CC against acute lymphoblastic leukaemia

XX Sequence 327 AA;

Query Match 44.6%; Score 749; DB 2; Length 327;

Best Local Similarity 47.3%; Pred. No. 1.2e-53;
 Matches 156; Conservative 63; Mismatches 105; Indels 6; Gaps 2;

QY 8 KLANVLLATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADLANVREGVQMGIAS 67
 DB 3 KLPNVLLATGTTAGAGASATGTGTGYAGALGVDTLLNAVPEVKLANVKGEOPSNMA 62
 QY 68 ESITNDLLKLASSVAELADSDVDGIVITHTDTLEETAYFLNVEKTKPIVVGSMR 127
 DB 63 ENMTGDVVLKLSQRNELLARDVDGIVITHTDTLEESAFIHLTVKSDKPVVVAAMR 122
 QY 128 PGTASADGMLNLYNAVAASNKDSRGKGLVTMNDIEIOGRDVSISINIKTEAFK-SAW 186
 DB 123 PATASADGPMNLLEAVVADGQSRGKGVVVLNDRIGSARYITKTNASTLDFEKABE 182
 QY 187 GPLGVVSGKSYWFRLLPAKHTVNSRPDIKQISLPQVDIAYSGVNTDTAYKALQNGA 246
 DB 183 GYLGVITGNRIYQNRIDKHTTTSVFPVRGLTSLPKVDIIYQDDPEYLDALIQGV 242
 QY 247 KALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSRQGGFVLRNAEQPDDKNDWVAHD 306
 DB 243 KGIYVAGAGSVSVRGIAGRKAMEKGVVIRSTRNGIV-----PPDEBLPELVDS 297
 QY 307 LNPOKARILAVAMTKTQDSKELORIFWY 336
 DB 298 LNPAPARILMLALTRTSDPKVIOEYFTY 327

RESULT 7

ID AAR70348 standard; protein, 348 AA.

XX AAR70348;

XX 25-MAR-2003 (revised)

XX 07-AUG-1991 (first entry)

XX Sequence of a protein with L-asparaginase (LA) activity in P4SN 30 or

XX P4SN 32.
 XX Enzyme; cancer therapy; leukaemia therapy.


```

XX OS Brwinia chrysanthemi.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /Label= signal
XX XX 22..348
XX PN EP211639-A.
XX XX
XX PD 25-FEB-1987.
XX PF 04-AUG-1986; 86EP-00305984.
XX PR 06-AUG-1985; 85GB-00019753.
XX XX
XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
XX PI Atkinson A, Minton NP, Gilbert HJ;
XX DR MPI, 1987-051784/08.
XX DR N-PSDB; AAN70557.
XX XX
XX PT New recombinant plasmids coding for L-asparaginase - esp. from Brwinia
XX PT carotovora, useful for treating malignancies and new transformed hosts.
XX PS Disclosure; Fig 4; 35pp; English.
XX XX
XX CC When E. carotovora SCRI 193 contg. plasmid pAGN 32 was cultured, the cell-
XX CC free culture broth contained 11.19 I.A. units/ml with specific activity
XX CC 53.34 units/mg of protein. These figures compare with 10.87 I.A. units/ml
XX CC and 14.97 units/mg of protein for the currently used prodn. strain
XX CC E. chrysanthemi NCPB 1066. (Updated on 25-MAR-2003 to correct PA field.)
XX XX
SQ Sequence 348 AA;

Query Match 44.6%; Score 749; DB 1; Length 348;
Best Local Similarity 47.3%; Pred. No. 1.3e-53;
Matches 156; Conservative 63; Mismatches 105; Indels 6; Gaps 2;

QY 8 KLANVYILATGGTIGAGSAAANSATYQAKVGVNKLINGVPELADIANVREGVQWQIAS 67
DB 24 KLPNIYILATGGTIGAGSAAATGTGTGKAGALGVDTLINAVPEVKLANVKGQFENMAS 83
QY 68 ESTINDDLKLAASVAELADSDVDGIVTTHGDTLEETAYFLNLTVEKTDKPIVVGSMR 127
DB 84 ENMTGDVVLKLSQRVNELARDDVDGVLTHTGDIYESAYFLHLTVKSDKPVVFAAMR 143
QY 128 PGTASADGMLNLNNAVAASNKDSRGKGLVTMNDIIOGRDVSINIKTEAFK-SAM 186
DB 144 PATASADGPMNLLEAVRVAAGDKQSRGVMVLANDRIGSARTITKTNASTLDTFFANEE 203
QY 187 GPLGMVBEKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKALAQNGA 246
DB 204 GYLGVIIIGRIYQNNIDKHLHTRSVFDVRGLTSLPKVDILYQODPEYLYDAALQHG 263
QY 247 KALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSQGGFVLRNABOPDDKNDVVAHD 306
DB 264 KGIIVYAGMGAGSVVGIAGMRKAMEKGVVIRSTRTGNGIV-----PDEBELPGLVSDS 318
QY 307 LNPQKARIILAVAMTKTQDSKEIQRIFWEY 336
DB 319 LNPQKARIILMLALTRTSDPKVIQIEYFHTY 348

RESULT 8
ABP98617 standard; protein; 348 AA.
AC ABP98617,
XX
XX DT 30-MAY-2003 (first entry)
XX

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DB OS Brwinia chrysanthemi L-asparaginase protein.
XX KM Asparaginase; cytostatic; blood; acute lymphoblastic leukemia.
XX OS Brwinia chrysanthemi.
XX OS WO2003018742-A2.
XX PN 06-MAR-2003.
XX PD 21-AUG-2002; 2002MO-RU000405.
XX PF 22-AUG-2001; 2001RU-00123442.
XX PR 04-APR-2002; 2002RU-00108505.
XX XX
XX PA (UCHR=) GOS UCHREZHDENIE NI INST BIOMED KHMITI.
XX PA (UCHR=) GOS UCHREZHDENIE TSENTR BIOINZHEMERIYA.
XX PI Bidarov MA, Zhgun AA, Gervaziev YV, Aleksandrova SS, Bogushev VG;
XX PI Sidoruk KV, Sveshnikova EV, Borisova AB, Omeinyuk NM, Archakov AI;
XX PI Skryabin KG, Sokolov NN;
XX DR MPI; 2003-268418/26.
XX XX
XX PT New isolated Brwinia carotovora L-asparaginase gene useful for producing
XX PT a L-asparaginase protein useful for treating malignant and nonmalignant
XX PT diseases of the blood.
XX PS Example 2; Page 9-10; 29pp; Russian.
XX XX
XX CC This sequence represents the complete form of an Brwinia chrysanthemi L-
XX CC asparaginase. The invention relates to the isolation of the gene and
XX CC protein for L-asparaginase from Brwinia carotovora and to the production
XX CC of the mature version of the protein especially by expression of the DNA
XX CC in a bacterial strain and has low affinity for L-glutamine. The protein
XX CC is useful for treating malignant and non-malignant diseases of the blood
XX CC (e.g. acute lymphoblastic leukemia)
XX XX
SQ Sequence 348 AA;

Query Match 44.6%; Score 749; DB 6; Length 348;
Best Local Similarity 47.3%; Pred. No. 1.3e-53;
Matches 156; Conservative 63; Mismatches 105; Indels 6; Gaps 2;

QY 8 KLANVYILATGGTIGAGSAAANSATYQAKVGVNKLINGVPELADIANVREGVQWQIAS 67
DB 24 KLPNIYILATGGTIGAGSAAATGTGTGKAGALGVDTLINAVPEVKLANVKGQFENMAS 83
QY 68 ESTINDDLKLAASVAELADSDVDGIVTTHGDTLEETAYFLNLTVEKTDKPIVVGSMR 127
DB 84 ENMTGDVVLKLSQRVNELARDDVDGVLTHTGDIYESAYFLHLTVKSDKPVVFAAMR 143
QY 128 PGTASADGMLNLNNAVAASNKDSRGKGLVTMNDIIOGRDVSINIKTEAFK-SAM 186
DB 144 PATASADGPMNLLEAVRVAAGDKQSRGVMVLANDRIGSARTITKTNASTLDTFFANEE 203
QY 187 GPLGMVBEKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGAVTDTAYKALAQNGA 246
DB 204 GYLGVIIIGRIYQNNIDKHLHTRSVFDVRGLTSLPKVDILYQODPEYLYDAALQHG 263
QY 247 KALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSQGGFVLRNABOPDDKNDVVAHD 306
DB 264 KGIIVYAGMGAGSVVGIAGMRKAMEKGVVIRSTRTGNGIV-----PDEBELPGLVSDS 318
QY 307 LNPQKARIILAVAMTKTQDSKEIQRIFWEY 336
DB 319 LNPQKARIILMLALTRTSDPKVIQIEYFHTY 348

RESULT 9
AAW98609 standard; protein; 364 AA.
XX
XX DT AAW98609
XX

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AAW98609;
 31-MAR-1999 (first entry)
 H. pylori GHPO 187 protein.
 GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
 peptic ulcer disease.
 Helicobacter pylori.
 WO9843478-A1.
 08-OCT-1998.
 01-APR-1998; 98WO-US006371.
 01-APR-1997; 97US-00833457.
 24-JUN-1997; 97US-00881227.
 29-JUL-1997; 97US-00902615.
 (INNR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 (HUMAN-) HUMAN GENOME SCI INC.
 Kleantous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;
 N-PSDB; AAX14328.
 MPI; 1998-542293/46.
 New isolated Helicobacter polynucleotides - used to develop products for
 the diagnosis, prevention and treatment of Helicobacter infections and
 gastrointestinal diseases.
 Claim 8; Page 1227-1229; 2054pp; English.
 This sequence represents a Helicobacter pylori GHPO protein of the
 invention. The polypeptides can be used for preventing or treating
 Helicobacter infections, and gastroduodenal diseases associated with
 these infections, including acute, chronic, and atrophic gastritis, and
 peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
 used for the production of antibodies. The products can also be used for
 detection and diagnosis

Query Match 42.7%; Score 717; DB 2; Length 364;
 Best Local Similarity 44.6%; Pred. No. 6.1e-51;
 Matches 148; Conservative 75; Mismatches 103; Indels 6; Gaps 5;

7 OKLANVVIATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADLANVGEQVMQ 66
 37 QNLPITALATGTTAGTSGANS-ASLSGYSNGELGIELKAIPLNRLARIQEQISNIG 95
 67 SSSITNDLLKLAASSVAELADSNVDGVIYTHGTDLLEBTAYFLNVEKTRPIYVGS 126
 96 SODMEERWFKAKRAQOELLIDSRIOGVYITHTDILBSAYFLNVLNSTRPVVLVGM 155
 127 RRGTMASADGMLNVAVVAASNKDSRGKGLVTMNDILOSGRDYSKINITEAPFSA- 185
 156 RRAASISADGALNVAASVVALNEKSAKNGVAVLMDNIFSAREVAKITHTTSTFKALN 215
 186 WGPLGAVVEGKSYWFLPAKRHTVNSEPDIKQISS-LPOVDIAYSXNVTTDAYKALAQ 244
 216 SGATSGVYVGTGRYVQPLRKHTTSESEFSLQKTPLPKVDIITHTAGMTPLPFOASLNS 275
 245 GAKALIHAGTNGSVSSRVVPALQELRKNGVQITRSSRQGGFTLRNAEQPDDKNDVYA 304
 276 HAKGVVIAGVGNGVSAGFLKAMQEASQMGVIVRSRVNSGBI--TSGEIDK-AFITS 332
 305 HDLNPOKARILLAMVAMTKTQDSKELQRIPEY 336
 333 DNLNPOKARVLLQALITKTNKEKIOEMPEEY 364

RESULT 10
 ABO61384
 ID ABO61384 standard; protein; 356 AA.
 AC ABO61384;
 29-JUL-2004 (first entry)
 Klebsiella pneumoniae polypeptide seqid 7901.
 Klebsiella pneumoniae polypeptide; transcription regulatory element;
 Recombinant expression vector; antibacterial; vaccine.
 Klebsiella pneumoniae.
 US6610836-B1.
 26-AUG-2003.
 27-JAN-2000; 2000US-00489039.
 29-JAN-1999; 99US-0117747P.
 (GENO-) GENOME THERAPEUTICS CORP.
 Breton GL, Osborne M;
 MPI; 2003-895346/82.
 N-PSDB; ACH94935.
 New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 preparing a vaccine composition against Klebsiella pneumoniae.
 Disclosure; SEQ ID NO 7901; 932pp; English.
 The invention describes a new isolated nucleic acid encoding a Klebsiella
 pneumoniae polypeptide. Also described are: a recombinant expression
 vector comprising the nucleic acid, operably linked to a transcription
 regulatory element; and a cell comprising the recombinant expression
 vector. The nucleic acid is useful for preparing a vaccine composition
 against Klebsiella pneumoniae. This is the amino acid sequence of a
 Klebsiella pneumoniae polypeptide of the invention

Query Match 42.3%; Score 711; DB 7; Length 356;
 Best Local Similarity 45.0%; Pred. No. 1.9e-50;
 Matches 150; Conservative 68; Mismatches 109; Indels 6; Gaps 2;

5 NOOKLANVVIATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADLANVGEQVMQ 64
 29 SETRLPHVILLATGTTAGTSGANSNTQGTGYKAGALGVOTLINAVPEMKIAHVEGEQVAN 88
 65 IASISITNDLLKLAASSVAELADSNVDGVIYTHGTDLLEBTAYFLNVEKTRPIYVVG 124
 89 IGSEMTSDIILQLSKRVNALLARDVDGVYITHTDILDETPYPLNTVSNKKEVFTFA 148
 125 SMRPGTMASADGMLNVAVVAASNKDSRGKGLVTMNDILOSGRDYSKINITEAPFSA 184
 149 AARPAITASADGPMMLLRAVTVVADPDARGKGVVAVLNDRIGAARFVTKINATSLDITRA 208
 185 -AMGPLGAVVEGKSYWFLPAKRHTVNSEPDIKQISS-LPOVDIAYSXNVTTDAYKALAQ 243
 209 PEEGYLVGVGKPKQFERVVDKIHRLRVFVYRQKVLPKVVIYGYDDPEYMDAALA 268
 244 NGAKALIHAGTNGSVSSRVVPALQELRKNGVQITRSSRQGGFTLRNAEQPDDKNDVYA 303
 269 HHADGIYAGTGAGSVRSAAIGIKKAOAGIVVRASTRSGV-----PDDSQPGIV 323
 304 AHDLPKARILLAMVAMTKTQDSKELQRIPEY 336
 324 ADSINPAKARILLMTALTQTKDPLIOQYFHTY 356

RESULT 11
ID ADF05106 standard; protein; 346 AA.
XX
AC ADF05106;
XX
XX 12-FEB-2004 (first entry)
DT
DE Bacterial polypeptide #1219.
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
OS Proteus mirabilis.
PN US6605709-B1.
PD 12-AUG-2003.
XX
XX 05-APR-2000; 2000US-00543681.
PF
PR 09-APR-1999; 99US-0128706P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
PI Breton GL;
XX
XX WPI; 2003-895291/82.
DR N-PSDB; ADF00934.
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 5391; 870pp; English.
XX
XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
XX Sequence 346 AA;
Query Match 42.3%; Score 710.5; DB 7; Length 346;
Best Local Similarity 46.2%; Pred. No. 26-50;
Matches 152; Conservative 58; Mismatches 114; Indels 5; Gaps 4;

9 LANVVLATGTTAGAGASANSATYQAAKVGVKLIAGVPELADLANVGEQWQIASB 68
22 LRVNVLATGTTAGAGGDS-ATSSSYTAGLGIIDLINNVEAKKYANLTGEVNVIGSQ 80
69 SITNDLLKLASSVAELADSNVDGIVITHGTDTLEETAYFLNLTVEKTKPIYVVGSKRP 128
81 DNVDDWMLKLANKIN--TTCDDKTDGVTITHTGTIMERTAYFLDLTTACKKPPVVMVGAMP 138
129 GTAMSDGMLNTYNAAVAVSNKDSRGKGVLTNNDLSGSDVSKSINIKTBKFSKA-WG 187
139 ARLGADGFLNLTNAAVAVSNDKASENRGVLTNNNSVISGKDVVKNNTTEVQAFQIYNG 198
188 PLGMVVEGKSYWFRLLPAKRTTVNSEPDIKQISLPOVDIAYSIGNVTDYAKYLAQNGAK 247
199 AGGYVADGKVVHYTYATTPR-ABKVAFDVSLTFLPVGIVYNNVANSDDLPAKAFINHRK 257

246 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSRQGGFVLNNAEQPDKDMVVAHDL 307
258 GIVSAGVNGNLYSDILNTLADGVKKGVVAVSRVPGFTTQNGEVDARKGFIASERL 317
308 NPQAKRIILAMVAMTKTQDSKELORIFWEX 336
318 NPQAKRVLLQLSLTETQDPATIQENPEKY 346
Db

RESULT 12
ID ABM68938 standard; protein; 348 AA.
XX
AC ABM68938;
XX
XX 20-NOV-2003 (first entry)
DT
DE Photorhabdus luminescens protein sequence #2035.
XX
XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX
XX Photorhabdus luminescens.
OS
XX WO200294867-A2.
PN
XX 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-1B003040.
PF
XX 07-FEB-2001; 2001FR-00001659.
PR
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taucrit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
XX WPI; 2003-148459/14.
DR
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
PT
XX Claim 2; SEQ ID NO 2035; 1205pp; French.
PS
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX
XX Sequence 348 AA;
Query Match 40.8%; Score 685.5; DB 6; Length 348;

Beet Local Similarity 44.1%; Pred. No. 2.4e-48; Matches 145; Conservative 65; Mismatches 114; Indels 5; Gaps 4;

QY 9 LANVVIATAGTITAGAGAAANSATYQAARKVGDKLIAGVPELADLANVRGEQWQIAE 68
 Db 23 LPNITLITATGTTIAGGSAIAGS-NYVAKRAVIDELVYANVPEIKIANIKGEQVVISGQ 81
 QY 69 BITNDLKLASSVAELADSNVDGIVITHGDTLEETAYFLNLVEKTDKPIVVGSMRP 128
 Db 82 DNMDOVWLTLAKRIN--ADCDKTDGVIITHGDTMEETAYFLDLTTHCKPIVVGAMRP 139
 QY 129 GTAMGADGMLNINNAVAVASNDKRGKGLVTMNDIEIGSDVSKSINKITAFKSA-WG 187
 Db 140 STALGADGFLNINNAVAVAGDTASAKRGVLMAMNDAVISGRVTVKSTTEVOAFQPVNAG 199
 QY 188 PLGMVVEGKSYMFRLPAKHHTVNSEFDIKQISLPQVDIAYSXGVTDTAYKALAONGAK 247
 Db 200 AEGFVHNGKVNRY-ADAKPRANKAIPDVSKDKLPKVGIVINYANASDLPAKALLKDGIO 258
 QY 248 ALIHAGTNGSVSSRVVPALELRKNGVQIIRSSROGGFVLNMAQPDNDKNDWVAHDL 307
 Db 259 GIVSAGVGNKNYKAIPTDLALAAKDGVVVRSRVPGVYVQDAEVDSDSKGFVASERL 318
 QY 308 NPQKARIILAMVAMTKTQDSKELORIFMEX 336
 Db 319 NPQKARVILQALITETRNPKIHEMFVKY 347

RESULT 13
 ABP98616 standard; protein, 326 AA.

AC ABP98616;
 XX
 DT 23-OCT-2003 (revised)
 DT 30-MAY-2003 (first entry)
 XX
 DE Mature Erwinia carotovora L-asparaginase.
 XX
 KW Asparaginase; cytosolic; blood; acute lymphoblastic leukemia.
 XX
 OS Pectobacterium carotovorum.
 XX
 PN WO2003018742-A2.
 PD 06-MAR-2003.
 PF 21-AUG-2002; 2002MO-RU000405.
 PR 22-AUG-2001; 2001RU-00123442.
 PR 04-APR-2002; 2002RU-00108505.
 XX
 PA (UCR=) GOS UCHREZHDENIE NI INST BIOMED KHMII.
 PA (UCR=) GOS UCHREZHDENIE TSENTR BIOINZHENERIYA.
 XX
 PI El'darov MA, Zhgun AA, Gervaziev YV, Aleksandrova SS, Bogush VG,
 PI Sidoruk KV, Sveshnikova EV, Borisova AA, Omeinyuk NM, Archakov AI,
 PI Skryabin KG, Sokolov NN,
 XX
 XX MPI, 2003-268418/26.
 DR
 XX
 PT New isolated Erwinia carotovora L-asparaginase gene useful for producing
 PT a L-asparaginase protein useful for treating malignant and nonmalignant
 PT diseases of the blood.
 XX
 PS Claim 4; Page 25-26; 29pp; Russian.
 XX
 CC This sequence represents the mature form of an Erwinia carotovora L-
 CC asparaginase. The invention relates to the isolation of the gene and
 CC protein for L-asparaginase and to the production of the mature version of
 CC the protein especially by expression of the DNA in a bacterial strain and
 CC has low affinity for L-glutamine. The protein is useful for treating
 CC malignant and non-malignant diseases of the blood (e.g. acute

CC lymphoblastic leukemia). (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 326 AA;

Query Match 40.3%; Score 677.5; DB 6; Length 326;
 Beet Local Similarity 45.0%; Pred. No. 1e-47; Indels 7; Gaps 3;
 Matches 149; Conservative 59; Mismatches 116;

QY 7 OKLANVVIATAGTITAGAGAAANSATYQAARKVGDKLIAGVPELADLANVRGEQWQIA 66
 Db 2 ENLPRIIVILATGTTIAGGSSQYANHWKAGALGVEITLIQVPELKTLANIKGEQVASIG 61
 QY 67 SBSITNDLKLASSVAELADSNVDGIVITHGDTLEETAYFLNLVEKTDKPIVVGSM 126
 Db 62 SENMTSDVLTLLTSKRVNELLARSDVDGIVITHGDTLDESYPFLNLTVKSDKPVVFCAS 121
 QY 127 RPTGMSADGMLNINNAVAVASNDKRGKGLVTMNDIEIGSDVSKSINKITAFKS-A 185
 Db 122 GNGNEV-PDGPMLNLGAQKVAADKNSRGRGLVVLNDRIGSARFISKTNALFTLDFKAE 180
 QY 186 WGPLGMVVEGKSYMFRLPAKHHTVNSEFDIKQISLPQVDIAYSXGVTDTAYKALAONG 245
 Db 181 EGYLGVIIGDKIYYQTRLDKXHTTRSVDVTVNVDKLPKVDIITGYQDDPEVWYDASISG 240
 QY 246 AKALIHAGTNGSVSSRVVPALELRKNGVQIIRSSROGGFVLNMAQPDNDKNDWVAH 305
 Db 241 VKGIYVAGMGAGSVSKRGDAGIRKASRKGIVVRSRYSRGIVPPDAGPG----LVAD 295
 QY 306 DLNPQKARIILAMVAMTKTQDSKELORIFMEX 336
 Db 296 SLSPKSRILMLALTKTNPAVADIDYFAY 326

RESULT 14
 ABP98615 standard; protein, 348 AA.

AC ABP98615;
 XX
 DT 23-OCT-2003 (revised)
 DT 30-MAY-2003 (first entry)
 XX
 DE Erwinia carotovora L-asparaginase.
 XX
 KW Asparaginase; cytosolic; blood; acute lymphoblastic leukemia.
 XX
 OS Pectobacterium carotovorum.
 XX
 PN WO2003018742-A2.
 PD 06-MAR-2003.
 PF 21-AUG-2002; 2002MO-RU000405.
 PR 22-AUG-2001; 2001RU-00123442.
 PR 04-APR-2002; 2002RU-00108505.
 XX
 PA (UCR=) GOS UCHREZHDENIE NI INST BIOMED KHMII.
 PA (UCR=) GOS UCHREZHDENIE TSENTR BIOINZHENERIYA.
 XX
 PI El'darov MA, Zhgun AA, Gervaziev YV, Aleksandrova SS, Bogush VG,
 PI Sidoruk KV, Sveshnikova EV, Borisova AA, Omeinyuk NM, Archakov AI,
 PI Skryabin KG, Sokolov NN,
 XX
 XX MPI, 2003-268418/26.
 DR
 DR N-PSDB; ABZ80801.
 XX
 XX
 PT New isolated Erwinia carotovora L-asparaginase gene useful for producing
 PT a L-asparaginase protein useful for treating malignant and nonmalignant
 PT diseases of the blood.
 XX
 PS Claim 1; Page 23-24; 29pp; Russian.
 XX

CC This sequence represents an *Erwinia carotovora* L-asparaginase encoded by
 CC a nucleotide sequence in plasmid pECAR-LANS. The invention also includes
 CC a homogeneous preparation of a mature form of L-asparaginase produced by
 CC expression of the DNA in a bacterial strain and has low affinity for L-
 CC glutamine. The protein is useful for treating malignant and non-malignant
 CC diseases of the blood (e.g. acute lymphoblastic leukemia). (Updated on 23
 CC -OCT-2003 to standardise OS field)

XX Sequence 348 AA;

Query Match 40.3%; Score 677.5; DB 6; Length 348;

Best Local Similarity 45.0%; Pred. No. 1.1e-47;

Matches 149; Conservative 59; Mismatches 116; Indels 7; Gaps 3;

QY 7 QCLANVILATGTTAGAGASANSATYQAAKGVKTLAGVPELADLANVNGEQYMOA 66
 DB 24 ENLPNVIATGTTAGAGSSQYANHWKAGALGVETLLQVPELTKTLNKEQYASIG 83
 QY 67 SESITNDLLKLAASVAELADSNVDGIYTHGTDTLEETAYPLNVEKTDKPIYVVGSM 126
 DB 84 SENMTSDVLLITLSKRVNELLARSDVDGVITHTGTDLDSPTPLNTYKSDKRVFCDS 143
 QY 127 RPTAMASADGMLNLVNAVAASNKDSRGKGVLTVMNDEIQSGRDVSKINIKTEAFKS-A 185
 DB 144 GNGNPV-PDGPMLYGAIVKVAADKNSRGKGVLVNDRIGSANFISKTNAFTLDFKAPD 202
 QY 186 NGPLGAVVEGKSYWFLPAKRTVNSEPDIKOISLPQVDIAYSIGNVDTAYKALAONG 245
 DB 203 EGYLGVIIDKTYQTRLDKRVHTRSVPFVTVNDKLPKVDIITYGDDEBYMDASIKRG 262
 QY 246 AKALIHAGTNGSVSSRRVVPALQELRNQVQIIRSSROCGFYLRAEOPDDKNDKMDV 305
 DB 263 VKGIVYAGAGASVSGSGDAGIRKASKGIIVVRSRSTSGIVPPDAGPG-----LVAD 317
 QY 306 DNPQKARIILAVAMTKTQDSKELORIPEY 336
 DB 318 SLSPAKSRILMLALFKTNPAVIOQYFAY 348

RESULT 15

ADO07179

ID ADO07179 standard; protein; 378 AA.

AC ADO07179;

DT 15-JUL-2004 (first entry)

DE Aspergillus oryzae asparaginase.

DE Asparaginase; enzyme; acrylamide; heat treatment; EC-3.5.1.1.

OS Aspergillus oryzae.

PN WO2004032648-A1.

PD 22-APR-2004.

PF 10-OCT-2003; 2003WO-DK000684.

PR 11-OCT-2002; 2002DK-00001547.

XX (NOVO) NOVOZYMES AS.

PI Budolfesen G, Jensen MT, Heldt-Hansen HP, Stringer MA, Lange L;

DR WPI, 2004-340772/31.

DR N-PSDB; ADO07178.

PT Preparing heat-treated product such as potato chips by providing raw
 PT material having carbohydrate, protein and water, treating raw material
 PT with enzyme reacting on asparagine or glutamine and heat treating to
 PT reduce water content.

PS Claim 9; SEQ ID NO 2; 46pp; English.

XX The present sequence is that of *Aspergillus oryzae* asparaginase. This
 CC enzyme shows optimal activity at pH 7 (at 37 degrees C) and 60 degrees C
 CC (pH 7.0) and is stable in the pH range from about 4.0 to 8.0. It has a
 CC molecular weight of 40-65 kDa (SDS-PAGE). N-terminal sequence showed 4
 CC different terminals, at amino acid positions 27, 30, 75 and 80 of the
 CC present sequence. A claimed method of reducing the formation of
 CC acrylamide during heat treatment of raw material comprising carbohydrate,
 CC protein and water involves treatment of the raw material with an enzyme
 CC prior to heat treatment. The enzyme may be an asparaginase, including A.
 CC oryzae asparaginase (optionally truncated to residues 27-378, 30-378, 75-
 CC 378 or 80-378), that is capable of reacting on asparagine or glutamine
 CC (optionally substituted). The method is useful for preparing a heat-
 CC treated product (claimed), such as potato products, potato chips,
 CC breakfast cereals, biscuits, roasted nuts, hot cakes, pancakes, etc.

XX Sequence 378 AA;

Query Match 35.9%; Score 602.5; DB 8; Length 378;

Best Local Similarity 43.1%; Pred. No. 2.1e-41;

Matches 143; Conservative 67; Mismatches 105; Indels 17; Gaps 10;

QY 9 LANVVIATGTTAGAGASANSAT--YQAAKGVKTLAGVPELADLANVNGEQYMOA 66
 DB 51 LNVVTFATGTT--AGSADNTATGYKAGAVGIQTLDVAPENLVANVAVGVTVNG 108
 QY 67 SESITNDLLKLAASVAELADSN--VDGIYTHGTDTLEETAYPLNVEKTDKPIYVVG 124
 DB 109 SPDITSIDILRLSKOINRVV--CNDPTMAGAVVTHGTDTLEESAFLDADVNGCRKPPVIVG 167
 QY 125 SRRPTAMASADGMLNLVNAVAASNKDSRGKGVLTVMNDEIQSGRDVSKINIKTEAFKS 184
 DB 168 AWPSTALSADGMLNLQSVTVAAASKARDKALVMDRIYSAPFASKTNANTVDTFA 227
 QY 185 -AWGPLGAVVEGKSYWFLPAKRTVNSEPDIKOISLPQVDIAYSIGNV--TDYAKALA 242
 DB 228 IEMGNLGEVSNKPYFFYPVK--PTGKTEVDIRNITSIRVDILVSYEDMHDLYSAL- 285
 QY 243 QNGAKALIHAGTNGSVSSRRVVPALQEL-RKNGVQIIRSSROCGFYLRAEOPDDKNDM 301
 DB 286 DNGAKGIVYAGSGSVSTPFSAMEDIYTKNIPVASTRGNGEVPSSA-----SSQ 340
 QY 302 VVAHDLNPOKARIILAVAMTKTQDSKELORI 333
 DB 341 IASGYLNPASKSRVLLGLLAQGSIEEMRAVP 372

Search completed: March 18, 2005, 21:32:35
 Job time : 171 secs

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OM protein - protein search, using SW model

Run on: March 18, 2005, 21:25:54 ; Search time 43 seconds

(without alignments)
583,304 Million cell updates/sec

Title: US-09-842-628-2

Perfect score: 1680
Sequence: 1 KEVENQOKLVAVILATGCT.....MVAMTKTQDSKELQRIFWY 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1680	100.0	336	5	PCT-US92-10421-2
2	1646.5	98.0	337	3	US-08-050-482A-2
3	1432.5	85.3	333	4	US-09-252-991A-22364
4	1063.5	63.3	374	4	US-09-328-352-6462
5	749	44.6	327	1	US-07-867-105B-1
6	711	42.3	356	4	US-09-489-039A-7901
7	710.5	42.3	336	4	US-09-543-681A-5391
8	372.5	22.2	333	4	US-09-134-000C-4613
9	361.5	21.5	332	4	US-09-710-279-1912
10	361.5	21.5	326	3	US-09-134-001C-3234
11	356	21.2	320	4	US-09-583-110-3586
12	356	21.2	321	4	US-09-107-433-3394
13	331.5	19.7	334	4	US-09-107-532A-4947
14	194	11.5	347	4	US-09-543-681A-8255
15	191.5	11.4	227	4	US-09-248-796A-17491
16	183	10.9	385	4	US-09-489-039A-7667
17	160.5	9.6	550	2	US-08-929-501-12
18	160.5	9.6	530	3	US-09-140-177-12
19	160.5	9.6	590	3	US-09-397-979-12
20	154	9.2	506	2	US-08-929-501-2
21	154	9.2	506	3	US-09-140-177-2
22	154	9.2	506	3	US-09-397-979-2
23	153.5	9.1	384	1	US-08-222-289-2
24	152	9.0	332	4	US-09-252-991A-25262
25	145.5	8.7	363	3	US-09-195-666A-4
26	145.5	8.7	363	3	US-09-635-705-4
27	145.5	8.7	363	4	US-09-634-858A-4

28	145.5	8.7	363	4	US-08-869-927C-4	Sequence 4, Appl1
29	145.5	8.7	565	3	US-09-008-481A-6	Sequence 5, Appl1
30	145.5	8.7	565	3	US-09-195-666A-5	Sequence 6, Appl1
31	145.5	8.7	565	3	US-09-195-666A-49	Sequence 49, Appl1
32	145.5	8.7	565	3	US-09-309-592-6	Sequence 6, Appl1
33	145.5	8.7	565	3	US-09-635-705-5	Sequence 5, Appl1
34	145.5	8.7	565	3	US-09-635-705-49	Sequence 49, Appl1
35	145.5	8.7	565	4	US-09-634-858A-5	Sequence 5, Appl1
36	145.5	8.7	565	4	US-08-869-927C-49	Sequence 49, Appl1
37	145.5	8.7	565	4	US-08-869-927C-5	Sequence 5, Appl1
38	145.5	8.7	565	4	US-08-869-927C-49	Sequence 49, Appl1
39	143	8.5	339	4	US-09-902-540-15220	Sequence 15220, A
40	126	7.5	365	3	US-09-195-666A-6	Sequence 6, Appl1
41	126	7.5	365	3	US-09-195-666A-7	Sequence 7, Appl1
42	126	7.5	365	3	US-09-635-705-6	Sequence 6, Appl1
43	126	7.5	365	3	US-09-635-705-7	Sequence 7, Appl1
44	126	7.5	365	4	US-09-634-858A-6	Sequence 6, Appl1
45	126	7.5	365	4	US-09-634-858A-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
PCT-US92-10421-2
Sequence 2, Application PC/TUS9210421
GENERAL INFORMATION:
APPLICANT: Robert, Joseph
APPLICANT: MacCallister, Thomas W
APPLICANT: Sethuraman, Natrajan
TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND
TITLE OF INVENTION: ITS USE IN ANTIVIRAL AND ANTICANCER THERAPY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSER: Banner, Birch, McKie and Beckett
STREET: 1001 G Street N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10421
FILING DATE: 19921204
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P4140003.8
FILING DATE: 04-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00100.41200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULAR TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
PCT-US92-10421-2
Query Match 100.0%; Score 1680; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.9e-149; Indels 0; Gaps 0;
Matches 336; Conservative 0; Mismatches 0;

QY 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDKLIAGVPELADLANVGE 60
DB 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDKLIAGVPELADLANVGE 60
QY 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 120
DB 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 120
QY 121 VVGSMPGTAMSDGMLNLVNAVAVASNKDSRGKGVLTWNDEIQSGRDVSKINIKTE 180
DB 121 VVGSMPGTAMSDGMLNLVNAVAVASNKDSRGKGVLTWNDEIQSGRDVSKINIKTE 180
QY 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 240
DB 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 240
QY 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 300
DB 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 300
QY 301 WYVAHDLPQKARILAMVAMTKTQDSKEIQRIFWEX 336
DB 301 WYVAHDLPQKARILAMVAMTKTQDSKEIQRIFWEX 336

RESULT 2

US-08-050-482A-2
Sequence 2, Application US/08050482A
Patent No. 6312939

GENERAL INFORMATION:
APPLICANT: ROBERTS, Joseph
MACALISTER, Thomas W.
SETHURAMAN, Natarajan

TITLE OF INVENTION: FREEMAN, Abbie G.
GENETICALLY ENGINEERED GLUTAMINASE AND
ITS USE IN ANTIVIRAL AND ANTICANCER THERAPY

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,482A

FILING DATE: 25-Apr-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US92/10421

FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 023032/0106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-050-482A-2

Query Match

98.0%, Score 1646.5, DB 3, Length 337,

Best Local Similarity 98.2%, Pred. No. 2.6e-146;
Matches 331; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDKLIAGVPELADLANVGE 60
DB 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDKLIAGVPELADLANVGE 60
QY 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 120
DB 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 120
QY 121 VVGSMPGTAMSDGMLNLVNAVAVASNKDSRGKGVLTWNDEIQSGRDVSKINIKTE 180
DB 121 VVGSMPGTAMSDGMLNLVNAVAVASNKDSRGKGVLTWNDEIQSGRDVSKINIKTE 180
QY 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 240
DB 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 240
QY 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 299
DB 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 300
QY 300 DWVAHDLPQKARILAMVAMTKTQDSKEIQRIFWEX 336
DB 301 DWVAHDLPQKARILAMVAMTKTQDSKEIQRIFWEX 337

RESULT 3

US-09-252-991A-22364
Sequence 22364, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22364
LENGTH: 393
TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22364

Query Match

Best Local Similarity 85.3%, Score 1432.5; DB 4; Length 393;
Best Local Similarity 84.3%, Pred. No. 4.3e-126;
Matches 284; Conservative 22; Mismatches 30; Indels 1; Gaps 1;

QY 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDKLIAGVPELADLANVGE 60
DB 1 KEVENOQKLANVVIATGTTAGAGASANSATYQAAYGVDPQULASVPQULDIANVGE 116

QY 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 120
DB 61 QMOJASBSITNDLLKLAASVAELADSDVDGIYTHGTDTLEETAFPLNVEKTDKPI 176

QY 121 VVGSMPGTAMSDGMLNLVNAVAVASNKDSRGKGVLTWNDEIQSGRDVSKINIKTE 180
DB 121 VVGSMPGTAMSDGMLNLVNAVAVADKARGGVLTWNDEILSGRDVSKINIKTE 236

QY 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 240
DB 181 AFKSAWGLGAVVEGKSYWFLPAKRHTVNSEFDIKQISSLPQVDIAYSIGNVDTAYKA 296

QY 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 299
DB 241 LAONGAKALIHAGTNGSVSSRVVPALQELRNKGVOIIRSSHVNGGQGFVLRNAEQPDDKN 356

QY 300 DNVVAHDLNPOKARILAMVAMTKTODSKELORIFMEY 336
 DB 357 DNVVAHDLNPOKARILAMVAMTKTODSKELORIFMEY 393

RESULT 4
 US-09-328-352-6462
 Sequence 6462, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 6462
 LENGTH: 374
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-6462

Query Match 63.3%; Score 1063.5; DB 4; Length 374;
 Best Local Similarity 64.7%; Pred. No. 1,9e-91;
 Matches 213; Conservative 45; Mismatches 68; Indels 3; Gaps 2;

QY 11 NVVILATGGTINAGASANSATYQAKVGVKLIAGVELDLANVRGEQVMOINSSEI 70
 DB 46 NVVVATGGTINAGASANSATYQAKVGVKLIAGVELDLANVRGEQVMOINSSEI 105
 QY 71 TNDLILKASSVAELADSDNDGIVTHTGDTLEETAYFLINVEKTRKIVVGSWRPCT 130
 DB 106 TDKELQARQVNEILKPKTVNGVVTHTGDTLEETAYFLINVEKTRKIVVGSWRPCT 165
 QY 131 AMSADGMLNLVNAVAVASNKDSRGKGLVTNDEIOSGDSVSKINIKTEAFKSAWGPUG 190
 DB 166 ALSADGPMNLVNAVAVASNKDSRGKGLVTNDEIOSGDSVSKINIKTEAFKSAWGPUG 225
 QY 226 TLVEGKPFYFRQSVKHTVASSEFNINIKGDLPTVQIYVGSMSLPDAVEAVAKAGAYA 285
 DB 249 LIHAGTNGSVSRVPALQELR-KGVQIILSSRQGGFVLRNAEQPDDKNDWVAHNL 307
 QY 286 ITHAGTNGSVSRVPALQELR-KGVQIILSSRQGGFVLRNAEQPDDKNDWVAHNL 345
 DB 308 NPOKARILAMVAMTKTODSKELORIFMEY 336
 QY 346 NPOKARILAMVAMTKTODSKELORIFMEY 374

RESULT 5
 US-07-867-105B-1
 Sequence 1, Application US/07867105B
 Patent No. 5310670
 GENERAL INFORMATION:
 APPLICANT: GOMARD, Christopher R.
 TITLE OF INVENTION: Improved Method for the
 TITLE OF INVENTION: Purification of Brwlnia
 TITLE OF INVENTION: L-Asparaginase
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Kirschelein, Oetinger, Israel
 ADDRESSES: & Schiefmiller, P.C.
 STREET: 551 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: NY 10176-0024
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch diskette

COMPUTER: Olivetti (IBM Compatible)
 OPERATING SYSTEM: MS DOS
 SOFTWARE: N1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/867,105B
 FILING DATE: 19920625
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9017002.8
 FILING DATE: 02-AUG-90
 ATTORNEY/AGENT INFORMATION:
 NAME: David B. Kirschelein
 REGISTRATION NUMBER: 17244
 REFERENCE/DOCKET NUMBER: -
 NAME: Alan Israel
 REGISTRATION NUMBER: 27564
 REFERENCE/DOCKET NUMBER: -
 NAME: Martin W. Schiefmiller
 REGISTRATION NUMBER: 30421
 REFERENCE/DOCKET NUMBER: -
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 a.a.
 TYPE: AMINO ACID
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: Polypeptide
 DESCRIPTION: The amino acid sequence of Brwlnia
 DESCRIPTION: chrysaanthemi L-asparaginase
 HYPOTHEICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Brwlnia chrysaanthemi
 US-07-867-105B-1

Query Match 44.6%; Score 749; DB 1; Length 327;
 Best Local Similarity 47.3%; Pred. No. 5.4e-62;
 Matches 156; Conservative 63; Mismatches 105; Indels 6; Gaps 2;

QY 8 KLANVILATGGTINAGASANSATYQAKVGVKLIAGVELDLANVRGEQVMOINSSEI 67
 DB 3 KLPNVILATGGTINAGASANSATYQAKVGVKLIAGVELDLANVRGEQVMOINSSEI 62
 QY 68 ESITNDLILKASSVAELADSDNDGIVTHTGDTLEETAYFLINVEKTRKIVVGSWRPCT 127
 DB 63 EMTGDTVLKASQVNEILKPKTVNGVVTHTGDTLEETAYFLINVEKTRKIVVGSWRPCT 122
 QY 128 PGTASADGMLNLVNAVAVASNKDSRGKGLVTNDEIOSGDSVSKINIKTEAFKSAWGPUG 186
 DB 123 PATASADGPMNLVNAVAVASNKDSRGKGLVTNDEIOSGDSVSKINIKTEAFKSAWGPUG 182
 QY 187 GFLGAVIGRITTYQRIDILATTRSVFDRGLTSLPKVDILVGYDDPEFLYDALIQHCV 242
 DB 183 GFLGAVIGRITTYQRIDILATTRSVFDRGLTSLPKVDILVGYDDPEFLYDALIQHCV 246
 QY 247 KALIHAGTNGSVSRVPALQELR-KGVQIILSSRQGGFVLRNAEQPDDKNDWVAHNL 306
 DB 243 KQIVVAGKAGSVSRVGLGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAGKAG 297

RESULT 6
 US-09-489-039A-7901
 Sequence 7901, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A

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Query Match	42.3%	Score 711	DB 4	Length 356
Best Local Similarity	45.0%	Pred. No. 2.3e-58		
Matches 150; Conservative	68;	Mismatches 109;	Indels 6;	Gaps 2

Qy		5	N O O K L A N V I L A T G C T I A D A G S A A N S A Y Q A A K G V E L I A G P E L A D I L A N V G E O V M Q	64
Dd		29	S E T R L P H I V I L A T G T I A G S A A S N Q T T G Y K A G I G V O T L I N A V E M S K I A H V E G Q V A N	88
Qy		65	I A B E S I T U N D L K L A S V A E L A D S N D V G I V T H T D T L E E F A P L N V E T D I P I Y V G	124
Dd		89	I G S E N N T S D I I L Q L S K R V A L L A R D D V D S V I T H T D T L D E P F L N I T V S N P V F T A	148
Qy		125	S M P G T A M S A D G M L A N Y N A V A A S N K D S R G K G V L T Y M D B I O S G R D V S K S I N I T B A F K S	184
Dd		149	A M R P A T A I S A D G P M N L L E A V T A A D P A D A G R G V M V L D R I G A A R F V T K N A T S L D T F R A	208
Qy		185	- A M P I C M V E G S Y F R L P A K R H Y N S F R D I K O J S L P O V D I A S Y G N V T D T Y K A L Q	243
Dd		209	P E E G Y I G V A V G P O P E T R V D K I H T L R S Y F D V R O L K V I P K V I I I Y G O D D E Y M D A I A	268
Qy		244	N G A K A L I H A G T N G S V S R V V P A L O E L R K N G V O I I R S S R O O G F V L R N A E O P D D K N D M V	303
Dd		269	H H A D G I I Y A G T A G S V S V S A A G I K K A Q O A G I V V R A S R T S G V V - - - - P P D S O G C L V	323
Qy		304	A H D N P O K A R I L A M V M T K O D S K E L O R I F E M Y	336
Dd		324	A D S L N P A K A R I L M T L T O K P O L Q I G O T P H T Y	356

RESULT 7

```

US-09-543-681A-5391
/ Sequence 5391, Application US/09543681A
/ Patent No. 6605709
/ GENERAL INFORMATION:
/ APPLICANT: GARY BRETON
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.1002-001
/ CURRENT APPLICATION NUMBER: US/09/543, 681A
/ CURRENT FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/128,706
/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 8344
/ SEQ ID NO 5391
/ LENGTH: 346
/ TYPE: PRT
/ ORGANISM: Proteus mirabilis
US-09-543-681A-5391

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Quest Match	42.3%	Score 710.5;	DB 4;	Length 346;
Best Local Similarity	46.2%	Pred. No. 2.4e-58;		
Matches 152;	Conservative 58;	Mismatches 114;	Indels 5;	Gaps 4;

QY 9 LANVLLTAGGTAGAGAAANSATQAAKAVVDKILNGVELADIANVREQYMOALASE 68
 Db 22 LRPVTLTAGGTAGGAGDS-ATSSSTYAGKGLDITLIINAVBEAKVNMLTBEQVNIISQ 80
 QY 69 SITNDLLKLASSVAELADSNVDGIVTHGTDLLEETAYPLNIVKTDKPIVVGSMRP 128
 Db 81 DMDQYWLKLANKIN--TDCKDTGDGVITHTGDIETETAYFLDITLACKKEVVVVGAMRP 138
 QY 129 GTAMSADGKLNILYNAYAVASNDGRSGKGLVLTMMDEIOSGADVSGKSIINIKETAKSLA-WG 187

Db	139	ATLADGDELNTLYNVAASDAKASNRGVLVTMNNSVTSGDVYKNNTEVOAQPINAG	198
Qy	188	PLGMVGEYSYMFRLPAKRHTVNSHFDIKQJSSLPOVDIAYSXGNTDIAVKLLAONGAK	247
Db	199	AQGYVHGDGVHYHTATPR-LEKFAFDVSKJTELPKGIYVNYNMAADLPKAFATIDHFK	255
Qy	248	ALTHAGTGKGSYSRVPALOEIRKNGVQIIRSRBOGGFYLRAAEOBDDKNDVVAHDL	3070
Db	258	GIYSAQVGNGLYSDILNTLADGVKKGVVVRSSRVPVGFVTQNGEYDADAKYFIASBRL	3177
Qy	308	NPOKARIILVAMTKTODSKELORIFMEY	336
Db	318	NPOKARVILQSLTETQDPATIQENFEKX	346

RESULT 8
ITE-09-13

```

Sequence 4613, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: LYNN DOUNETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134.000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055.778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4613
LENGTH: 333
TYPES: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4613

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Query Match	22.2%	Score 372.5;	DB 4	Length 333;
Best Local Similarity	30.0%	Pred. No. 1,3e-26;		
Matches 105; Conservative	67;	Mismatches 137;	Indels 41;	Gaps 11

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Qy 4 ENOKRANVILATGGTIA---GAGASAA-----NSATQAKVGVDKLIAGVPELADLAN 56
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 QRRKQKHTLVVHTGGTISMSKVAGGSVAHREKHPMBQBA-----LFGSKVLY---- 52

Qy 57 VRGEQVMQJASSITNDDLLKLASSVAELADSNVDGIVITRGHTDTEBETAPYPLANVEKT 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 53 --VEDIFENPSPHMTLERMFOLKERI--QKAASEPIDGVVITHGDTLEETAPYFLDITLEK 1090
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Qy 117 DKETVAVGSMREPGTAMSDGMLNTYNAAVAASNKDSRGKGLVYMANDEIOSGRVDSKISIN 1767
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 110 KIPITVLTGMRSSNEIGSDGLYNFISAIWTAQSPDSYDKGLVYMANDEIHATRAYVTKTHT 1698
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Qy 177 IKTRAPKS--AMRPLGVNVBEGKSYNWRLLPARKHTYNSEBDIKQISLSPQVDIANSYGWTD 2355
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 TNVAFRTPTFPDPTGILAKERAPF---AKVLLPQBVCDVSSVKG--NVHVVAKVAGMB 2233
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 236 TAYKALQNGAALTLHAGTNGSVSSRVVPLAOLERKNGVQIITSSRQOGGFVLRNABOP 2955
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 RMEELLNTPETDGLVIALGAGNLPETPLPALQKMLDNGIPVVLVSRCSNGI-----AEDI 2799
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 296 DD-----KNDVYVAHDLNPOKARILANVAVMTKTQDSRELORIITWEX 336
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 280 YDAGGSGVGLKMGVVPFARGINGPARRLLVGLNSENKPELKEB--PLEH 328
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RESULT 9

US-09-710-279-1912
Sequence 1912, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P0348005

CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1912
LENGTH: 322
TYPE: PRN
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-1912

Query Match 21.5%; Score 361.5; DB 4; Length 322;
Best Local Similarity 27.6%; Pred. No. 1.4e-25;

Matches 92; Conservative 73; Mismatches 151; Indels 17; Gaps 6;

QY 9 LANVVIATGTITAGAGAAASATYQAANKGVGDKLIAGVPELADLANVRGQVQJASB 68
DB 1 MKRLIHTGTITISQDQTNKVTINENPISQHONI-----ISQYAEVDEINLNTIPSP 55
QY 69 SITNDLLKLASSVAELADSNVDGIVITHGDTLEETAYFLNVEKTDKPIVWGSNRP 128
DB 56 HMTISNVRLRDEIITYSKENIYDGFVITHGDTLEETAFLLDLIDIOEPVITGAMS 115
QY 129 GTAMGADGMLNLYNAVAVASNDKSRGKGLVTMNDIEOSGRDVSINIKTEAFKSA-WG 187
DB 116 SNEISGSDGLYNFTISAIRVASSSEAHKGVWVFNDIEHTARAVTKHTSINTPQSPNOG 175
QY 188 PLGVNVEGKSYWFLPAKHTVNSSEPDIKQISLPQVDIAYSYGNTDPAAYALQNGAK 247
DB 176 PLGVNVEGKSYWFLPAKHTVNSSEPDIKQISLPQVDIAYSYGNTDPAAYALQNGAK 229
QY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSSRQGGFV-----LRNAQPPDDKNDWV 303
DB 230 GIVIEALGGGNLPKSCINGLQOCLKKNIPLVVSRFNGIYSPVAYABEGGADLKNNGVI 269
QY 304 -AHDLPQKARILAMVAMTKTODSKELQRIEWE 335
DB 290 FENGLNGPRARLKLVLGSLQDWTQNLERYFER 322

RESULT 10

US-09-134-001C-3234
Sequence 3234; Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3234

LENGTH: 326

TYPE: PRN

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3234

Query Match 21.5%; Score 361.5; DB 3; Length 326;
Best Local Similarity 27.6%; Pred. No. 1.4e-25;

Matches 92; Conservative 73; Mismatches 151; Indels 17; Gaps 6;

QY 9 LANVVIATGTITAGAGAAASATYQAANKGVGDKLIAGVPELADLANVRGQVQJASB 68
DB 5 MKRLIHTGTITISQDQTNKVTINENPISQHONI-----ISQYAEVDEINLNTIPSP 59

QY 69 SITNDLLKLASSVAELADSNVDGIVITHGDTLEETAYFLNVEKTDKPIVWGSNRP 128
DB 60 HMTISNVRLRDEIITYSKENIYDGFVITHGDTLEETAFLLDLIDIOEPVITGAMS 119
QY 129 GTAMGADGMLNLYNAVAVASNDKSRGKGLVTMNDIEOSGRDVSINIKTEAFKSA-WG 187
DB 120 SNEISGSDGLYNFTISAIRVASSSEAHKGVWVFNDIEHTARAVTKHTSINTPQSPNOG 179
QY 188 PLGVNVEGKSYWFLPAKHTVNSSEPDIKQISLPQVDIAYSYGNTDPAAYALQNGAK 247
DB 180 PLGVNVEGKSYWFLPAKHTVNSSEPDIKQISLPQVDIAYSYGNTDPAAYALQNGAK 233
QY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSSRQGGFV-----LRNAQPPDDKNDWV 303
DB 234 GIVIEALGGGNLPKSCINGLQOCLKKNIPLVVSRFNGIYSPVAYABEGGADLKNNGVI 293
QY 304 -AHDLPQKARILAMVAMTKTODSKELQRIEWE 335
DB 294 FENGLNGPRARLKLVLGSLQDWTQNLERYFER 326

RESULT 11

US-09-583-110-3586

Sequence 3586; Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PAT00-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3586

LENGTH: 320

TYPE: PRN

ORGANISM: Streptococcus pneumoniae

US-09-583-110-3586

Query Match 21.2%; Score 356; DB 4; Length 320;
Best Local Similarity 31.6%; Pred. No. 4.4e-25;

Matches 102; Conservative 51; Mismatches 134; Indels 36; Gaps 8;

QY 12 VTIATGCTTA-GAAGAAASATYQAANKGVGDKLIAGVPELADLANVRGQVQJASB 70
DB 5 IIVHTGTITISQDQASGAVVTSNDPMNHNPNLEGI-----QVHALDFENLPSPHI 57
QY 71 TNDLLKLASSVAELADSNVDGIVITHGDTLEETAYFLNVEKTDKPIVWGSNRP 130
DB 58 KKKMLVLYKTKESAD-NTDGVYTHGDTLEETAFLLDLIDIOEPVITGAMS 115
QY 131 AMSADGMLNLYNAVAVASNDKSRGKGLVTMNDIEOSGRDVSINIKTEAFKSA-AMGEL 189
DB 116 BLGSDGVNLYSALALVAVASDDRAADKGLVVMNDIEHTARAVTKHTSINTPQSPNOG 175
QY 190 GNVVVEGKSYWFLPAKHTVNSSEPDIKQISLPQVDIAYSYGNTDPAAYALQNGAK 249
DB 176 GLIMKOELIYFTABPR-----VRFDLNHIQGI--VPITSAVAGMTDELIDMLDLERHLDL 229
QY 250 IHAAGTNGSVSRVVPALQELRKNGVOIIRSSR-----QGGFVLRNAQPPDD 297
DB 230 IIGAGAGNIPKETAOKLESLLQKGIIPVALVSRCENGIAEPYAYOGGAVQLQKA----- 284
QY 298 KNDVVAHDLPQKARILAMVAM 320
DB 285 --GVFFVKEINQAKRLKLLIAL 305

RESULT 12

US-09-107-433-3394

; Sequence 3394; Application US/09107433

; Patent No. 6800744

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN

; THERAPEUTICS

; NUMBER OF SEQUENCES: 5206

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: <Unknown>

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: <Unknown>

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,433

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/ 085131

; FILING DATE: May 12, 1998

; APPLICATION NUMBER: 60/051553

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-011

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 3394:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 321 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus pneumoniae

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...321

; SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

US-09-107-433-3394

Query Match 21.2%; Score 356; DB 4; Length 321;

Best Local Similarity 31.6%; Pred. No. 4,4e-25;

Matches 102; Conservative 51; Mismatches 134; Indels 36; Gaps 8;

QY 12 VVLTATGTTA-GAGASANSATYQAAGVVDKLIAGVELADLANVREGVQMOJASEI 70
DB 6 ILVHTGTTISQADSGAVVTSSDPMNHNPNLEGI-----QVHALDFENLPSPHI 58
QY 71 TDDDLKLASSVAELADNDVDGIYTHGDTLEETAYFLNVEKTDKPIVVGSMRPGT 130
DB 59 KKKHMLVLYOKKERAD-NYOGVYTHGTDTLEETAYFLDMEVPHMFIYLTGAMRSN 116
QY 131 AMSADGMLTNAVAVASNKDSRGKGLVTNMDIEIQSGDVSKSINIKTEAFKS-AMGEL 189
DB 117 ELGSDGVVYVYALRAVASDRAADKGLVVMNDEIHAAYVTKHTTNNVFQTPTHGPL 176
QY 190 GNVGSGKSWFELPAKRTVNSEPDIKQSSLPQVDIANSYGAVTDTAYKALANGAKRL 249
DB 177 GLIMKOEILYFTAEPR---VRFIDHIOGL--VPIISAYAGMTDELIDMLDLRLDGL 230

RESULT 13

US-09-107-532A-4947

; Sequence 4947; Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 4947:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...334

; SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

US-09-107-532A-4947

Query Match 19.7%; Score 331.5; DB 4; Length 334;

Best Local Similarity 28.2%; Pred. No. 9,4e-23;

Matches 95; Conservative 65; Mismatches 142; Indels 35; Gaps 9;

QY 8 KLANVVIATGTTAGAGASANSATYQAAGVVDKLIAGVELADLANVREGVQMOJAS 67
DB 12 KKKHMLVLYOKKERAD-NYOGVYTHGTDTLEETAYFLNVEKTDKPIVVGSMR 67
QY 68 ESITNDDLLKLASSVAELADNDVDGIYTHGDTLEETAYFLNVEKTDKPIVVGSMR 127
DB 68 PHIMPSHLVLEKRIIS-AVAGISGVVYTHRTDTLEETAYFLDITIGKCLPIVLTGMR 126

QY 128 PGTAMADGMLNLYNAVAASNDKSGVLTWNDEIOSGRDYSKINIKTEAFKS-AW 186
 DB 127 SGNELSGDGLYNPESAIRVASCEBALDKVLYVWDEIHSAKYVTHHTTNATPTPTPL 186
 QY 187 GFLGAVVEKSYWFR--LPKCHTNSBFDIKOISLPOVDIAYSYGAVTDAKALAN 244
 DB 187 GPICGVTYKRIIFLOBLLETKR-----LDISAVDG--TIPYKAYAGMOGDLLEIAHT 238
 QY 245 GAKLIHAGTNGSVSRVVPALQELRKNGVOIIRSR-----QGGFVLRAA 292
 DB 239 KYDGLVTEALAGNLPPOALALEKLVKIPVLSRCPNGIAEPVYDEGGKEL--- 295
 QY 293 EOPDDKNVVAHDINPQKARILAMVAMTKTODSKEL 329
 DB 296 ----EKMGIIFCNSINSQKARVLLAVVYGLSGEHL 328

RESULT 14

US-09-543-681A-8255
 / Sequence 8255, Application US/09543681A
 / Patent No. 6605709
 / GENERAL INFORMATION:
 / APPLICANT: GARY BRETON
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 / FILE REFERENCE: 2709.1002-001
 / CURRENT APPLICATION NUMBER: US/09/543,681A
 / CURRENT FILING DATE: 2000-04-05
 / PRIOR APPLICATION NUMBER: US 60/128,706
 / PRIOR FILING DATE: 1999-04-09
 / NUMBER OF SEQ ID NOS: 8344
 / SEQ ID NO 8255
 / LENGTH: 347
 / TYPE: PRT
 / ORGANISM: Proteus mirabilis
 / US-09-543-681A-8255

Query Match 11.5%; Score 194; DB 4; Length 347;
 Best Local Similarity 24.2%; Pred. No. 8.3e-10;

Matches 75; Conservative 58; Mismatches 123; Indels 54; Gaps 13;

QY 11 NVVILATGTTAGASAAASATYQAAKGVDKLJAGVPEL--ADLANVR-GEQWQIAS 67
 DB 12 SIYVYVTGTT---GMQSHDHG-YIPVSGHLQRLAKMPEFRBEMPNFTIKHPLIDS 67
 QY 68 BITNDLKLASSVAELADSDVDGIVYTKGTDLLEETAYFLN-LVEKTDKPIYVVGSM 126
 DB 68 SNITPBDWQSIADDIS--NYCHYDGFVILAGDTMAFTASALSFMEGLAKPVIYVTSQ 125
 QY 127 RGTAMASADGMLNLYNAVAASNDKSGVLTWNDEIOSGRDYSKINIKTEAFKSAM 186
 DB 126 IPELALRSQCTNLNALTITAAHPT--NEVALPFNNNTLYRG--NRALKAHADGFA-- 178
 QY 187 GFLGAVVEKSYWFR--LPKCHTNSBFDIK--QISLPO-----VDIAYSY 230
 DB 179 -----PASPNGAPLLEAGINIKTFINPLPKKGFIAHHTTPQIGVITY 225
 QY 231 GAVTDTAYALANAKALI--HAGTNGSVSRVVPALQELRKNGVOIIRSR----- 282
 DB 226 PGLSBEVVNKKIIMQPKALILRSYGVGNAPSHPALSTIREATRGVVVNLQICISGRV 285
 QY 283 QGGFVLRAA 292
 DB 286 NMGGYATGQA 295

RESULT 15

US-09-248-796A-17491
 / Sequence 17491, Application US/09248796A
 / Patent No. 674137
 / GENERAL INFORMATION:
 / APPLICANT: Keith Weinstein et al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

QY 147 ASNKDSRGKGLVWVNDKIOSGRDYSKINIKTEAFKS-AMGFLGAVVEKSYWFRPLPAK 205
 DB 1 ASNRSRGRGVIALNDRISSGFYITKSNANSLDTPKISGGYGVGNFVNNRIYPPPPAK 60
 QY 206 -----RHTVNSER-----DIKQISLPOVDIAYSYGAVTDAKALAN-GAK 247
 DB 61 PGLTMTFHINDLFSSSYVYALGNDI--IPCLPEVTIYAHQGLNNEIFKFIYNDLKSX 118
 QY 248 ALIHAGTNGSVSRVVPALQELRKNGVOIIRSRQGGF-----VLRNAP- 293
 DB 119 GIILATMGAGSMDTNOYLSDLINPNPPIYYSKRSMDGVPPISLPKVLAVIKDAAD 178
 QY 294 ---QPDKN---DWVVAHDINPQKARILAMVAMTKTODSKELORIF 333
 DB 179 NKGPATKVPFVNAIAGTYLNPQKARILQLCLNGBMDLSKINVF 224

Query Match 11.4%; Score 191.5; DB 4; Length 227;
 Best Local Similarity 29.2%; Pred. No. 7.2e-10;

Matches 66; Conservative 39; Mismatches 80; Indels 41; Gaps 9;

Search completed: March 18, 2005, 21:34:11
 Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2005, 21:26:43 ; Search time 141 Seconds
(without alignments)
787.673 Million cell updates/sec

Title: US-09-842-628-2

Perfect score: 1680
Sequence: 1 KEVENOQKLANVITATGTT.....MVAMTKQPSKELQRIWEX 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/US09_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppa/US09_PUB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1680	100.0	336	US-09-842-628-2
2	758	45.1	375	US-10-406-025-2
3	717	42.7	364	US-09-882-227-84
4	356	21.2	320	US-10-472-928-4160
5	251	14.9	335	US-09-738-626-5846
6	127.5	7.6	548	US-10-369-493-513
7	114	6.8	544	US-10-282-122A-65021
8	113	6.7	544	US-10-282-122A-65715
9	113	6.7	723	US-10-282-122A-60463
10	113	6.7	1862	US-10-282-122A-49757
11	112	6.7	543	US-10-282-122A-64156
12	110.5	6.6	313	US-09-738-626-5967
13	110.5	6.6	330	US-10-781-014-504

14	110.5	6.6	545	US-10-282-122A-47225	Sequence 47225, A
15	110	6.5	540	US-10-369-493-181	Sequence 181, App
16	110	6.5	550	US-10-282-122A-50017	Sequence 50017, A
17	109.5	6.5	1574	US-10-695-499-179	Sequence 179, App
18	109.5	6.5	1978	US-10-695-499-60	Sequence 60, App
19	109.5	6.5	1981	US-09-928-457-38	Sequence 38, App
20	109.5	6.5	2015	US-10-066-551-1	Sequence 1, App
21	109.5	6.5	2015	US-10-282-122A-65772	Sequence 65772, A
22	109	6.5	423	US-10-437-965-147620	Sequence 147620, A
23	109	6.5	540	US-10-282-122A-74161	Sequence 74161, A
24	109	6.5	540	US-10-472-928-3964	Sequence 3964, App
25	109	6.5	641	US-10-267-311-51	Sequence 51, App
26	108.5	6.5	255	US-10-296-115-766	Sequence 766, App
27	108.5	6.5	540	US-10-282-122A-57926	Sequence 47926, A
28	108	6.4	542	US-10-369-493-10295	Sequence 10295, A
29	107	6.4	1057	US-10-282-122A-70305	Sequence 70305, A
30	107	6.4	1057	US-10-470-048B-152	Sequence 152, App
31	107	6.3	390	US-10-282-122A-57094	Sequence 67094, A
32	106.5	6.3	390	US-10-406-686A-32	Sequence 32, App
33	106.5	6.3	714	US-09-841-786-4	Sequence 4, App
34	106.5	6.3	3241	US-09-841-786-1	Sequence 1, App
35	106.5	6.3	3241	US-10-647-057-1	Sequence 1, App
36	106.5	6.3	543	US-10-282-122A-53595	Sequence 63595, A
37	106	6.3	4150	US-09-808-880-2	Sequence 2, App
38	106	6.3	4150	US-09-969-362-1	Sequence 1, App
39	105.5	6.3	923	US-10-282-122A-49854	Sequence 49854, A
40	105.5	6.2	2457	US-10-282-122A-71468	Sequence 71468, A
41	105	6.2	449	US-10-282-122A-43762	Sequence 43762, A
42	105	6.2	3413	US-10-042-665A-8	Sequence 8, App
43	105	6.2	6281	US-09-815-242-12996	Sequence 12996, A
44	104.5	6.2	10498	US-10-470-048B-440	Sequence 440, App

ALIGNMENTS

RESULT 1
US-09-842-628-2
Sequence 2, Application US/09842628
Patent No. US2002064862A1
GENERAL INFORMATION:
APPLICANT: ROBERTS, JOSEPH
APPLICANT: MACALLISTER, THOMAS W.
APPLICANT: SETHIRAMAN, NARARAJAN
APPLICANT: FREEMAN, ABIE G.
TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
FILE REFERENCE: 023032/0108
CURRENT APPLICATION NUMBER: US/09/842,628
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 08/050,482
PRIOR FILING DATE: 1995-04-25
PRIOR APPLICATION NUMBER: PCT/US92/10421
PRIOR FILING DATE: 1992-12-04
PRIOR APPLICATION NUMBER: DE P 4140003.8
PRIOR FILING DATE: 1991-12-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 336
TYPE: PRT
ORGANISM: Pseudomonas sp.
US-09-842-628-2

Query Match 100.0%; Score 1680; DB %; Length 336;
Best local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVENOQKLANVITATGTTAGAGSANSATYQAAKGVNDLNGVPELDLNAVRE 60
DB 1 KEVENOQKLANVITATGTTAGAGSANSATYQAAKGVNDLNGVPELDLNAVRE 60

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QY 61 QWQJASESITNDLLKLAASVAELADSNVDGIVITHTGDTLEETAYELNVEKTDKPI 120
DB 61 QWQJASESITNDLLKLAASVAELADSNVDGIVITHTGDTLEETAYELNVEKTDKPI 120
QY 121 VVVGSRPCTASADGMLNNAVAASNDKSRGKGVLYTMNDEIOSGRDVSKEINIKTE 180
DB 121 VVVGSRPCTASADGMLNNAVAASNDKSRGKGVLYTMNDEIOSGRDVSKEINIKTE 180
QY 181 AFKSAWPGFMVVEGKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGVTDTAYKA 240
DB 181 AFKSAWPGFMVVEGKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGVTDTAYKA 240
QY 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSROGGFVLRNAEQPDDKND 300
DB 241 LAQNGAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSROGGFVLRNAEQPDDKND 300
QY 301 WYVAHDLPQKARILAMVMTTQDSKELQRIFWEX 336
DB 301 WYVAHDLPQKARILAMVMTTQDSKELQRIFWEX 336

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RESULT 2

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US-10-406-025-2
/ Sequence 2, Application US/10406025
/ Publication No. US20030186380A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20030186380A1ozymes Biotech, Inc.
/ APPLICANT: Thomas, Michael D.
/ TITLE OF INVENTION: Method for producing secreted polypeptides having L-asparaginase
/ FILE OF INVENTION: activity
/ FILE REFERENCE: 10289,200-US
/ CURRENT APPLICATION NUMBER: US/10/406,025
/ PRIOR FILING DATE: 2003-04-01
/ PRIOR APPLICATION NUMBER: US 60/369,192
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 2
/ LENGTH: 375
/ TYPE: prt
/ ORGANISM: Bacillus subtilis
US-10-406-025-2

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Query Match 45.1%; Score 758; DB 14; Length 375;
Best Local Similarity 47.6%; Pred. No. 5,6e-57;
Matches 158; Conservative 58; Mismatches 112; Indels 4; Gaps 3;

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QY 6 QOKLANVILATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADIANYRGEQWQI 65
DB 47 KQDLPIRILATGGTTAGADQSTSTTEYKAGVGVESLIEAVPEKDIANYSGEQIVNV 106
QY 66 ABEISTNDLLKLAASVAELADSNVDGIVITHTGDTLEETAYELNVEKTDKPIYVGS 125
DB 107 GSTINDKLLKLAARINHLASDDVDGIVITHTGDTLEETAYELNVEKTDKPIYVGS 166
QY 126 MRPGTMSADGMLNNAVAASNDKSRGKGVLYTMNDEIOSGRDVSKEINIKTEAFKS- 184
DB 167 MRPSTIASDGBSNLYNAKVAAPAKKGTLYVNDIJAARYTKNTTTIDFISSE 226
QY 185 AWGLPMVVEGKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGVTDTAYKALAN 244
DB 286 GAKGIVFPASSGNGSLSDAEKAGDSAVKGVTVVSRTRGNGVTPNQYAE--KDLAS 343
QY 245 GAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSROGGFVLRNAEQPDDKNDVYA 304
DB 305 HDLNPQKARILAMVMTTQDSKELQRIFWEX 336
QY 344 NSLNPQKARILAMVMTTQDSKELQRIFWEX 375
DB 344 NSLNPQKARILAMVMTTQDSKELQRIFWEX 375

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RESULT 3

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US-09-882-227-84
/ Sequence 84, Application US/09882227
/ Publication No. US20030158396A1
/ GENERAL INFORMATION:
/ APPLICANT: Kleanthous, Harold
/ APPLICANT: Al-Garawi, Amal
/ APPLICANT: Miller, Charles
/ APPLICANT: Tomb, Jean-Francois
/ APPLICANT: Oomen, Raymond P.
/ TITLE OF INVENTION: Identification of Polynucleotides
/ TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in the
/ FILE REFERENCE: 06132/047002
/ CURRENT APPLICATION NUMBER: US/09/882,227
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: US 08/902,615
/ NUMBER OF SEQ ID NOS: 638
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 84
/ LENGTH: 364
/ TYPE: prt
/ ORGANISM: Helicobacter pylori
US-09-882-227-84

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Query Match 42.7%; Score 717; DB 10; Length 364;
Best Local Similarity 44.6%; Pred. No. 1,9e-53;
Matches 148; Conservative 75; Mismatches 103; Indels 6; Gaps 5;

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QY 7 QOKLANVILATGTTAGAGASANSATYQAAKVGVDKLIAGVPELADIANYRGEQWQI 66
DB 37 ONLPITALATGTTAGAGAS-ASIGSYSGELGKELKAIPLNRLARIGSEQISNIG 95
QY 67 SESITNDLLKLAASVAELADSNVDGIVITHTGDTLEETAYELNVEKTDKPIYVGS 126
DB 96 SODMNEBWFYKLRQGLDSDRIQGVITHTGDTLEESAFPLNLRSTKPVVLVGM 155
QY 127 MRPGTMSADGMLNNAVAASNDKSRGKGVLYTMNDEIOSGRDVSKEINIKTEAFKS- 185
DB 156 RNAASLSADGMLNNAVAASNDKSRGKGVLYTMNDEIOSGRDVSKEINIKTEAFKS- 215
QY 186 WGLPMVVEGKSYWFLPAKHTVNSEFDIKQISLPQVDIAYSYGVTDTAYKALAN 244
DB 216 SGATISVYGGKTRYYMQPLRKHTTESSEFSLQKLPKVIITHTAGTIDLPQASINS 275
QY 245 GAKALIHAGTNGSVSSRVVPALQELRKNGVQIIRSSROGGFVLRNAEQPDDKNDVYA 304
DB 276 HAKGVVINGVNGVNSAGFLKAMQASQGVIVVSSVNSGEI--TSGEIDDK-AFITS 332
QY 305 HDLNPQKARILAMVMTTQDSKELQRIFWEX 336
DB 333 DNLNPQKARVLLQALATKTNKKEKIQEMFEEX 364

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RESULT 4

```

US-10-472-928-4160
/ Sequence 4160, Application US/10472928
/ Publication No. US20050020813A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
/ TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE: P026926WO
/ CURRENT APPLICATION NUMBER: US/10/472,928
/ PRIOR FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: GB-0107658.7
/ NUMBER OF SEQ ID NOS: 4979
/ SOFTWARE: SeqMan99, version 1.03
/ SEQ ID NO 4160
/ LENGTH: 320
/ TYPE: prt

```


ORGANISM: Streptococcus pneumoniae
FEATURE:
OTHER INFORMATION: L-asparaginase, putative
OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15903854 (0.E+01)
US-10-472-928-4160

Query Match 21.2%; Score 356; DB 17; Length 320;
Best Local Similarity 31.6%; Pred. No. 2, 7e-22;
Matches 102; Conservative 51; Mismatches 134; Indels 36; Gaps 8;

QY 12 VVILATGGTGA-GAGASAAASATYQAAYGVDKLIAGVPELADLANVRGEQVMOJASESI 70
DB 5 ILVLTGGTISQWADSGAVTSSDPMHNSVPLEGI-----QVHALDFNLPSPI 57
QY 71 TNDLLKLASSVAELADSDVDGIVITHTGDTLEETAYFLNLVEKTDKPIYVVGSRPBT 130
DB 58 KPKHMLVLYQKKEED--NYDGVVITHTGDTLEETAYFLDMEVPHMIVLTGARSSN 115
QY 131 AMSADQMLNLYNAVAVASNKSGRGKGLVTMNDIISGRDVSINIKTEAFKS-AMGPTL 189
DB 116 ELGSDGVVYLSALRYASDDRADKGVAVVMDIHAAYTKHTTTNSTQTPTPHGPTL 175
QY 190 GNVGEGSYWFLPAKRTVTNSEFDIKQISLPQVDIAYSYGNTDTAYKALAONGAKAL 249
DB 176 GLIMQELIYFTYABR-----VRFDLDHIGL--VPIISAYGMTDELIDMLDLBHLDEL 229
QY 250 IHAGTNGSVSSRVVPALQELKNGVQITRSSR-----QQGFTLRNMQPDD 297
DB 230 IIAQAGANGIPKRTAQKESLLQKGPVALVSRFCNGIAPVYAYGGGVOLQKA----- 284
QY 298 KNDWVAHDNPOKARIILAMVAM 320
DB 285 --GVFFVKELNMQARKLILAL 305

RESULT 5

US-09-738-626-5846
Sequence 5846; Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5846
LENGTH: 325
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5846

Query Match 14.9%; Score 251; DB 9; Length 325;
Best Local Similarity 26.2%; Pred. No. 3, 4e-13;
Matches 75; Conservative 53; Mismatches 120; Indels 38; Gaps 6;

QY 12 VVILATGGTGAAGASAAASATYQAAYGVDKLIAGVPELADLANVRGE--QVMOJASES 69
DB 22 VAVITTTGGT--ACSDANNGHLLPTVS--GAD--TLAPIPAFRGAQIAFEIHINLSDSS 77
QY 70 TNDLLKLASSVAELADSDVDGIVITHTGDTLEETAYFLNLVEKTDKPIYVVGSRMG 129
DB 78 KTFEDLDSIIATVHVLYLBDPVDVGVVTHGDTSMESBALAVDTFLDDPRLVFTGAQKEP 137
QY 130 TMSADQMLNLYNAVAVASNKSGRGKGLVTMNDIISGRDVSINIKTEAFKSAMGPTL 189
DB 138 DHPEDGPNLPEACLIADSPSARGIIGALIVGHAIVIPAKGCY----- 181
QY 190 GNVGEGSYWFLPAKRTVTNSEFDIKQISLP-----QVDIAYSYGNTDTAYKALA 242
DB 182 -----MHTSDELAPATNGPESPBPDDALPAVKLADVSEIIPAYGATGATVBAAI 232
QY 243 ONGAKALIHAGTNGSVSSRVVPALQELKNGVQITRSSRQGGGV 288
DB 233 AAGAGLVLEAMSGSVGSRMGDALGKALDAGIPVYMSTRVBRGEV 278

RESULT 6

US-10-369-493-513
Sequence 513; Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 513
LENGTH: 548
TYPE: PRT
ORGANISM: Deinococcus radiodurans
US-10-369-493-513

Query Match 7.6%; Score 127.5; DB 15; Length 548;
Best Local Similarity 19.8%; Pred. No. 0.035;
Matches 94; Conservative 70; Mismatches 146; Indels 165; Gaps 21;

QY 1 KEVENOQKLVN-----VILATGGTGAAGASAA-----SATYQAK 38
DB 57 KEVELDQKLVNIGAOULKEVASKTMNDITGDTTITVYGAQIVKGLRVNAAANPLAK 116
QY 39 VGVDDKLIA-GVPELADLANVRGEQVMOJASESITNDLLKLASSVAELADSDVDGIV 96
DB 117 RQIDRAVNAVAIIEIKKLAVSDESEAIKKVAGISANDE--TVGQELASMDKVGEGVIT 174
QY 97 ---THTGDT-----LEETAYFL-----NL----- 112
DB 175 IEESSGFTDEVVDVVEGMQFDKFINPYFTNPEKMAVLEDAVYIINEKKSINLMDMLPV 234
QY 113 ---VEKTDKPIYVVGSRMGTA--DGMNLNLYNAVAVASNKSGRGKGLVTMND 163
DB 235 LERVAQOTGRPLILINADVEGELATLVNKLKGLTNI--AAVKAGFGGRKREMLRDI-A 291
QY 164 RIQSGRDVSKSINIKTEAFKSAMGPTL-----VVEGKSYWFLPAK 206
DB 292 AVTGERVVSSEDGHTLE-----NVGEMELGRAARIRITKQETITVQKGRQAQIDARV 344
QY 207 HTVNSEFDI-----KOISLPQVDIAYSYGNTDTAYKAL-----AONGAKAL 249
DB 345 NAIKELDSTDSDVAREKLOERLAKISGCVAVIRVGAATETELKEKGRHYEDALSTARSA 404

Qy 250 IHAG--TANGSVSSRVVLPALQELRN-----GVOI-----IRSSROGGFVL 289
Db 405 VEEGIIVAGGGTTLRLVTPVRKRAASLTGDEATGARILRLALEBPARGIAANAGEGSVI 464
Qy 290 RRAEPPDK-----NDWVVAHDLPOR-----ARILAMVMTX 322
Db 465 VNAVVGSDKARYGFMNATGEYVEDVMAAGIVDPARTALONMAISGILLITTE 519

RESULT 7

US-10-282-122A-65021
Sequence 65021, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65021
LENGTH: 544
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65021

Query Match 6.8%; Score 114; DB 15; Length 544;
Best Local Similarity 19.2%; Pred. No. 0.51;
Matches 80; Conservative 61; Mismatches 130; Indels 146; Gaps 19;

Qy 1 KEVENOQKLANV-----VILATGGINAGAS-----AASATYQA-----K 38
Db 58 KEIKLKDFENNAQGVKAVSKTNDVAGDTTATVLAQSVAGMKVTVGNMPTDIK 117
Qy 39 VGVDKILAG-VPELADLANV--RGEQVQIASESITNDILKLASSVAELADSDVDGIV 95
Db 118 RGIDDAVALVELKNIKAKPCPTSKKIAQVGSISANSDB--QVGAIIAEAMKRGKRGVI 175
Qy 96 ITHGDTLLE-----TAYPLNVER-----TDKPIVQSGMRPGTAMSADG 136

Db 176 TVEDEKSLLENLDVEGQDFRGVISPFIINDAEKQIAGLNDPVLDPDK--ISNIRD 232
Qy 137 MLNLVNAVAVASN-----KDSRGKGLVTVNNDIQSGRDVSXSINIKTEAF----- 182
Db 223 LLPVLEQVAKSRPLLIITAEVGEALATLVNNI--RGILKIVAVAPGEGDKRKML 289
Qy 183 -----KSANGPIGM-----VVEGKSYPRLPK----- 205
Db 290 QDIALITGVVISERVGLSEKATLDLQAKRIEIKENTTVIDFGDADAQIEARVAEI 349
Qy 206 ---RHTVNSRD-----IKQISLPQVDIAVSYGNVTD--AYKALQN 244
Db 350 ROQIETATSDYDKELQGRVAKLAGVAIVVGAATFVEMKCKORVEDALHATPAAYE 409
Qy 245 GAKALIHAGTNGSVSSRVVLPALQELRN-----GVOIIRSSROGGFVLMAEQP 295
Db 410 GVVA-----GGVALLFARAALENTLHGNDQDAGVQI-----VLRVAVSP 450

RESULT 8

US-10-282-122A-65715
Sequence 65715, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65715
LENGTH: 544
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-10-282-122A-65715

Query Match 6.7%; Score 113; DB 15; Length 544;
Best Local Similarity 18.9%; Pred. No. 0.62;
Matches 79; Conservative 62; Mismatches 130; Indels 146; Gaps 19;

Qy	1	KEVENOQIKLVN-----VILATGGVIAAGAS-----AANSATYQAA-----K	38
Db	58	KEIELDKPENMAQWKEVASKTNDVADGTTTATVLAQSVABEGKCTVYAGNPPTDK	117
Qy	39	VGVDKLIAG-VPELADLVANV-RGEQWQJABESITNDLLKLASSVAELADSNVDGIV	95
Db	118	RGIDKVAVALVEELKNIYAKPCOTSKEIAQVGSISANSDE-QVGAIIAEAKKEVKEGVI	175
Qy	96	ITHGTDTLEE-----TAYPLALVEK-----TDKPIYVGSNAPPTGAMSADG	136
Db	176	TVEDGKSLNEBLDVESGQFDRGYLSPYFINDAEQIAGLNDPFLATLDPDK---ISNIRD	233
Qy	137	MLNLYNNAVAVASN-----KDSRGKVLVTNNDKIEOSGDVYSKNITTEAF-----	182
Db	233	LLEFVLEQVAKASRPLLIINAEVDEGKALATLVVNNI---RGIIKTYAVAAAPGQBRKAML	288
Qy	183	-----KSAWQPLGM-----VVEGKSYWFLRLPAK-----	205
Db	290	QDIAILTGTGTVIBSEVGLSLEKATLTDLQAKRIEIGKENTTIIDGFDQAQIEARVAEI	345
Qy	206	---RHYNSFPD-----IKQISLPEVDIAVSYGNVTDI---ATKALAQN	244
Db	350	RQOIEATSPDYDBKLOEBRVAKIAGGVAIVKGAATEVEMKEKORVADALHATRAAVER	408
Qy	245	GARALITHAGNGSVSSRVVPAOLOLRKN-----GVOIIRSSRQGGFVLRNREP	295
Db	410	GVVA-----GGGVALIRARALLENLHNSNDQDAGVCI-----VIRAVESP	450

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RESULT 9
US-10-282-122A-60463
Sequence 60463, Application US/10262122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haebebeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ERTA.034
CURRENT APPLICATION NUMBER: US/10/0282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/250,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1

```

```

; SEQID NO 60463
; LENGTH: 723
; TYPE: PRF
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60463

```

Query Match	6.7%	Score	113	DB	15	Length	723
Best Local Similarity	22.8%	Pred. No.	0.94				
Matches	74	Conservative	56	Mismatches	111	Indels	84
						Gaps	17

[illegible]

RESULT 10
US-10-282-122A-49757
Sequence 49757, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITTA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
Prior APPLICATION NUMBER: 60/191,078
Prior FILING DATE: 2000-03-21
Prior APPLICATION NUMBER: 60/206,848
Prior FILING DATE: 2000-05-23
Prior APPLICATION NUMBER: 60/207,727
Prior FILING DATE: 2000-05-26
Prior APPLICATION NUMBER: 60/230,335
Prior FILING DATE: 2000-09-06
Prior APPLICATION NUMBER: 60/230,347
Prior FILING DATE: 2000-09-09
Prior APPLICATION NUMBER: 60/242,578
Prior FILING DATE: 2000-10-23
Prior APPLICATION NUMBER: 60/253,625
Prior FILING DATE: 2000-11-27
Prior APPLICATION NUMBER: 60/257,931
Prior FILING DATE: 2000-12-22
Prior APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 49757
 ; LENGTH: 1862
 ; TYPE: PRF
 ; ORGANISM: Burkholderia fungorum
 ; US-10-282-122A-49757

Query Match 6.7%; Score 113; DB 15; Length 1862;
 Best Local Similarity 22.9%; Pred. No. 3.6;
 Matches 78; Conservative 47; Mismatches 102; Indels 114; Gaps 16;

QY 15 LATGTTAGAGSA-ANSTYQAAYGVKLAGVPELADLVNVEQVQJASISITND 73
 DB 1044 LNAAGTTGGVGLAAGNATLTS---GRDPTDLTG-----SLRGATITGAGSGSTPA 1092
 QY 74 DLKLAASVAELADSNVDGIVITHTDTLEETAYFLNVEKDKPIYVVGSMRPGTAMS 133
 DB 1093 DV--QAGSTALTASNDVLTGTLAGSTVALTA-----GQDVVNSGTLQ---SSS 1138
 QY 134 ADGMLNVAVAASNKOSRGK-GVL-----VTNDEIQSGRDV----- 171
 DB 1139 DTNLALYSGVGVTSVNSGALNTVLAGTDINLGGTTVALDPTLQASADVAVVTSLSGQ 1198
 QY 172 -----SKSINIKTEAFKSAMGPL--GMVVEKSYWFLPARHIVNSEFDIK 216
 DB 1199 GNGFVTAGNIGAGSLAPAGSAVLNAGATISQGGILIQGVN----- 1240
 QY 217 QISLPQVDIAVSYGNTDTAYKALAQ-----NGAKALIH--GTGNGSV----- 259
 DB 1241 QVSAIGNVAV---NNIESTSLASAGTSGSGSLTVNGAALAAAITATANGDVTVA 1296
 QY 260 -----SSRPVALQELRNQVQIIRSSHQGGFVLNRNQ 294
 DB 1297 GDLAAGTVGTALNDIN-----VAGATISNGDAVLNMQ 1331

RESULT 11
 US-10-282-122A-64156
 ; Sequence 64156, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Foreyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 64156
 ; LENGTH: 543
 ; TYPE: PRF
 ; ORGANISM: Mycoplasma pneumoniae
 ; US-10-282-122A-64156

Query Match 6.7%; Score 112; DB 15; Length 543;
 Best Local Similarity 20.0%; Pred. No. 0.76;
 Matches 83; Conservative 52; Mismatches 131; Indels 148; Gaps 18;

QY 1 KEVENQKLANV-----VILATGTTAGAGSANSATYQAAYGVKLAGVPELADL 54
 DB 57 KEIETDPLENIGAKVISVAAVSTNDIAGDGTITTAIAGETNRGVAVNNG---AMP 112
 QY 55 ANVR-----GEQVQJASISITNDLKLASSVAELADSNV 91
 DB 113 VNVRGIDASQILITELDKRSKKINTMBEIQVAALSSGKEIGKLAQAMALVGNK-- 170
 QY 92 DGIIVTHTDTLEET-----AYFLNVEK---TDKPIVVV----- 123
 DB 171 -GVITTDPAKINTITLETGIEFKGYASPYMSDQKMEVLDQPIVLVSAMKINTIK 229
 QY 124 -----GSMRPG-----TAMSDGMLNVAVAASNK--DSRGKGV-- 158
 DB 230 EILPLBSGMEGNPLIADPDPAEEVVTTLAVNGLRGTINVAACKNBYGKQALLED 289
 QY 159 -----VTNDEIQSG-RDYSKSIKITEAFKSAMGFLGMVVEKSYWFLPARHIVN 210
 DB 290 LAISGTALVNNELGGFKDV--TVNHGELARV-----QVAKETTVIGSGSKETIQ 341
 QY 211 SEFDI-----KOISLPQVDIAVSYGNTDTAYKAL-----AONGA 246
 DB 342 KHLDLNGLKQTEKTYDTLKERIAHLISQVAVVRVGATETLAQKELKRIEDALNST 401
 QY 247 KALIHAG--TGNGSVSSRPVALQELR-----KN-----GVQIIRSS 281
 DB 402 KAAVEGIIISGGIALNVSTIINDSKLADYKAKETSAMNKLKILVGEIYAKS 455

RESULT 12
 US-09-738-626-5967
 ; Sequence 5967, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIYAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162

/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: JP 00/280988
/ PRIOR FILING DATE: 2000-08-03
/ NUMBER OF SEQ ID NOS: 7059
/ SOFTWARE: PatentIn ver. 3.0
/ SEQ ID NO 5967
/ LENGTH: 313
/ TYPE: PR
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-5967

Query Match 6.6%; Score 110.5; DB 9; Length 313;
Best Local Similarity 22.0%; Pred. No. 0.46;
Matches 69; Conservative 53; Mismatches 120; Indels 71; Gaps 15;

QY 15 LATGTTAGAGSAAASATYQAAKGVVDKLT-----AGPELADLAN 56
DB 3 LASCSSDSSDSTSDAGDSYRVGINQLVQHPALDAATTGPKAFBAGVDVTFDEQN 62
QY 57 VAGEQ-----VMOJASBSITNDLLKLAASVAELADSNVD-GIVTHTDTLLESTAYF 109
DB 63 ANGEQGTALTTSQCFASDNL--DLVLAVALTPAQAQTQNTIDIPVLFATVD-----AVS 115
QY 110 LNLVEKTDKPIYVVGSMRPGTAMSA--DQMLNLYNAVAASNKDSRGKGLVTMNDLQIS 167
DB 116 AELVDSNEAP-----GGNTVGTSDIAPTEQQLLELLQGLV----PDAKSIGI-VYASGEVNS 166
QY 168 GBDVKSINIKTEAFKASANGPIGMYVEGKSYFRLPAKHNTNSEPDQK-ISSLPOVDI 226
DB 167 -----QVQVDEYTKAEPPLGLSV-----NTQYVTVNRIQAAVEALGDVDV 207
QY 227 AY-SYGNVTVDTAVKLAONGAKALYHA-GTNGSVSSRVVPAQLGRKNGVQIISSRQ 284
DB 208 IYVPTDNMVSIGISLVQVAEQKQIPVIGASGTVGEGALATL-----GIDYTELGKQT 261
QY 285 GGFVLRNAEQPDD 297
DB 263 GEMALRIIQDGED 274

RESULT 13
US-10-781-014-504
/ Sequence 504, Application US/10781014
/ Publication No. US20040180408A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompeju, Markus
/ APPLICANT: Kroege, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
/ FILE REFERENCE: BGI-126CPN
/ CURRENT APPLICATION NUMBER: US/10/781,014
/ PRIOR FILING DATE: 2004-02-17
/ PRIOR APPLICATION NUMBER: US 09/602,740
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: 60/141,031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 60/143,208
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 60/151,572
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19931412.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931413.6
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931419.5
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931420.9
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931424.1

/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931428.4
/ PRIOR FILING DATE: 1999-07-08
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 784
/ SEQ ID NO 504
/ LENGTH: 330
/ TYPE: PR
/ ORGANISM: Corynebacterium glutamicum
US-10-781-014-504

Query Match 6.6%; Score 110.5; DB 16; Length 330;
Best Local Similarity 22.0%; Pred. No. 0.5;
Matches 69; Conservative 53; Mismatches 120; Indels 71; Gaps 15;

QY 15 LATGTTAGAGSAAASATYQAAKGVVDKLT-----AGPELADLAN 56
DB 20 LASCSSDSSDSTSDAGDSYRVGINQLVQHPALDAATTGPKAFBAGVDVTFDEQN 79
QY 57 VAGEQ-----VMOJASBSITNDLLKLAASVAELADSNVD-GIVTHTDTLLESTAYF 109
DB 80 ANGEQGTALTTSQCFASDNL--DLVLAVALTPAQAQTQNTIDIPVLFATVD-----AVS 132
QY 110 LNLVEKTDKPIYVVGSMRPGTAMSA--DQMLNLYNAVAASNKDSRGKGLVTMNDLQIS 167
DB 133 AELVDSNEAP-----GGNTVGTSDIAPTEQQLLELLQGLV----PDAKSIGI-VYASGEVNS 183
QY 168 GBDVKSINIKTEAFKASANGPIGMYVEGKSYFRLPAKHNTNSEPDQK-ISSLPOVDI 226
DB 184 -----QVQVDEYTKAEPPLGLSV-----NTQYVTVNRIQAAVEALGDVDV 224
QY 227 AY-SYGNVTVDTAVKLAONGAKALYHA-GTNGSVSSRVVPAQLGRKNGVQIISSRQ 284
DB 225 IYVPTDNMVSIGISLVQVAEQKQIPVIGASGTVGEGALATL-----GIDYTELGKQT 278
QY 285 GGFVLRNAEQPDD 297
DB 279 GEMALRIIQDGED 291

RESULT 14
US-10-282-122A-47225
/ Sequence 47225, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ PRIOR FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47225
LENGTH: 545
TYPE: PRT
ORGANISM: Borrelia burgdorferi
US-10-282-122A-47225

Query Match 6.6%; Score 110.5; DB 15; Length 545;
Best Local Similarity 18.0%; Pred. No. 1;
Matches 73; Conservative 68; Mismatches 131; Indels 133; Gaps 17;

QY 1 KEVENOQKLANV-----VILATGTTAGAGASANSATTGAQKGVNDKLIAGVPELA- 52
DB 57 REIELENPENNGAQLKEVALKT-NDVAGDGTATATVLAIAABEGKNVSSGINPIGI 115
QY 53 -----DLANVRGEQVWQIASISITNDLKLAS-----SVAELADNDVDGIYI 96
DB 116 KKGIDHVAVLAIAEKIRQSAKKTITKEEIAQVASISANDSYIGEKIAEMDKVGDGYIT 175
QY 97 THGDTLEET-----AYF-----LNL 112
DB 176 VEESKTFDITISYVGMQPDRCGLSPYFSTNKNSVNEDDAFILIYEKKISSIKELLPV 235
QY 113 VEK-----TDKPIYVGSMPRTAMSDGMLNTYNAVAVASNKD-----SRGKGLVTMNDI 165
DB 236 LEKVLGTNPFLIIMADIEGDALALVNSVRGALVCAIKSPGGRKAKMLDI-AVL 294
QY 166 QSGRDVSKSINKTEAFKSAWGPLGVVE--GKSYWFLPAKRTV---NSEPDIKQIS 219
DB 295 TGGVLAISEELGLTLEVE-----IQQLGQAKTIKVDKONTTIIINTGKE-QIKERS 344
QY 220 SLPPVDI-----AYSQNTDTIYKAL-----AQNGAKAL 249
DB 345 ELIKQIEDSTSEYDEKLOERLAKLVGVAVINVAIVTEVELEKKEHREVDALSATRAA 404
QY 250 IHAGT--GNGSVSRVVPALQEL-----RKNGQIIRSRQ 284
DB 405 VEEGVVPGGGSTLIEVAMTLDITITSKLSYEEKQGEIVKSLER 449

RESULT 15
US-10-369-493-181

Sequence 181, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 181
LENGTH: 540
TYPE: PRT
ORGANISM: Xenorhabdus nematophilus
US-10-369-493-181

Query Match 6.5%; Score 110; DB 15; Length 540;
Best Local Similarity 18.8%; Pred. No. 1.1;
Matches 85; Conservative 73; Mismatches 141; Indels 154; Gaps 20;

QY 1 KEVENOQKLANVILATGTTAGAGASANSATTQAA----- 37
DB 58 REIELEDPENM-----GAQVKEVASRADAAGDGTATVLAQSYTEGLKAVAGMN 112
QY 38 ----KVGVDK-LIAGVPELADLANVRGQ--WQIASISITNDLKLASSVAELADSN 90
DB 113 PMDLKRGIDKAVIAAVERBKLSVPCSDSTIAQVGTISANSDE--TYGKLIABMDKYG 170
QY 91 VDGIV-ITHGDTLEB-----TAYPLNT----- 112
DB 171 KEQVITVEGTGLEDELVDVEGMQPDRCGLSPYFINKPEAGSILENPIYILLVDKISNI 230
QY 113 -----VEKTKPIYVGSMPRTAMSDGMLNTYNAVAVASNK-----DSRGKGLV 159
DB 231 RELPLVEIGVAKASKPLVIAEDVEGEMATLVVNMNGIVKVAVKAPEGDRKAKMLQ 290
QY 160 TMNDEIOSGRVSKSINKTEAFKSAWGPLG-----HVEGKSYWFLPAK-- 205
DB 291 DI-ATLNGTVISEIGLEB--KATLEDLQAKRIYINKOTTTIIDVGEMAAIAAYT 347
QY 206 --RHTV---NSEFD-----IKQISSLPQVDIAYSQNVDT--AYKALA 242
DB 348 QIROQIEESTSDYDEKLOERLAKLVGVAVIKGAATEVEKKEKRAVDDALHATRAAV 407
QY 243 QNG-----AKALIHGTGNG--SYSRVPLQELRKNGVITIISSRQGGFV 288
DB 408 EGVVAGGVALVRAAAIISALTGDNEDQNVGIRV--ALRAMBAPMROIIVENAGEPSV 465
QY 289 LRNAE-----QPDKNDWVAHDLPK 311
DB 466 VNVKASQNGHGYNAATEYGDMEIMGLDPTK 498

Search completed: March 18, 2005, 21:36:39
Job time : 144 secs

A28063 (EC 3.5.1.38) - Acinetobacter calcoaceticus
N:Alternate names: glutaminase-asparaginase
C:Species: Acinetobacter calcoaceticus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A28063
R:Tanaka, S.; Robinson, B.A.; Appella, E.; Miller, M.; Ammon, H.L.; Roberts, J.; Weber, J. Biol. Chem. 263, 8583-8591, 1988
A>Title: Structures of amidohydrolases. Amino acid sequence of a glutaminase-asparaginase hysanthemi.
A:Reference number: A28063; MUID:88243706; PMID:3379033
A:Accession: A28063
A:Molecule type: protein
A:Residues: 1-331 <TAN>
A:Cross-references: UNIPROT:P10172
A>Note: the source is designated as Acinetobacter glutaminasificans
C:Superfamily: asparaginase
C:Keywords: hydrolase

Query Match 61.8%; Score 1037.5; DB 1; Length 331;
Best Local Similarity 62.0%; Pred. No. 2,2e-63;
Matches 204; Conservative 52; Mismatches 70; Indels 3; Gaps 2;

QY 11 NVVILATGGTIGAGASANSATYQAKYGVDTLIGVPELADLANVRSQVMOQIASBI 70
DB 3 NVVIVATGGTIGAGASSTNSATYSNAKVPVDALIKAVQVNDLANITIGIQALQVASEBI 62
QY 71 TNDLILKLASSVAELADSDVDGIVTHTGDTLLEAFYPLNVEKTDKPIVVGSRPPT 130
DB 63 TDKELSLARQVNDLVKPSVGVVITHTGDTMEERAFPLNVEKTDKPIVVGSRPPT 122
QY 131 AMSADGMLNLVNAVAVASNKDSRGKGVLTVMDEIOSGRDVSINIKTEAFKSAWGPFG 190
DB 123 ALSADGPLNLVAVALLASSENKAKNGVWLWDSIFPAADVTGKINIHHTAFTVSGWALG 182
QY 131 MYVEGSKYWFRLPAKHTVNSEPDIKQI--SLPQVDIAVSYGNTDTYKALQNGAKA 248
DB 183 TLVEGKPYWFRSSVKKGTNNSEFNIEKIQGDALPGQIYVGSDDNMPDAPVQAFKAGVYA 242
QY 249 LTHAGTNGSVSSRVVPAQLQELR-KNGVQIIRSSRQGGFVLRNAEQPDDKNDVVAHDL 307
DB 243 LTHAGTNGSMANVLPVPRKLDHDEGLQIVRSSRVAGFVLRNAEQPDDKIGWIAHDL 302
QY 308 NPQKRIILAMVAMTKTQDSKELQRIFWEX 336
DB 303 NPQKRIILMALATTKTNDAKEIQNMFNXY 331

RESULT 3
B5953
periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain H
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B5953
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimelantia, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A55480; MUID:21074935; PMID:11206551
A:Accession: B5953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <STO>
A:Cross-references: UNIPROT:O8XC2; GB:AB005174; NID:G12517506; PIDN:AA058088.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
A:Gene: ansb
C:Superfamily: asparaginase

Query Match 46.8%; Score 786; DB 2; Length 348;
Best Local Similarity 48.3%; Pred. No. 3.2e-46;
Matches 159; Conservative 59; Mismatches 107; Indels 4; Gaps 3;

QY 9 LANVILATGGTIGAGASANSATYQAKYGVDTLIGVPELADLANVRSQVMOQIASB 68
DB 23 LPNITILATGGTIGAGGSATRS-NYTAGKGVENLVNAVQQLDIANVKGQVNNISQ 81
QY 69 SITNDLILKLASSVAELADSDVDGIVTHTGDTLLEAFYPLNVEKTDKPIVVGSRP 128
DB 82 DMNDVWVTLTKKIN--TDCCKTQGFVTHGDTMEERAFPLDVLVCKDKPVMWGANRP 139
QY 129 GTAMSADGMLNLVNAVAVASNKDSRGKGVLTVMDEIOSGRDVSINIKTEAFKSA-WG 187
DB 140 STMSADGPFNLVNAVAVTAAKASANRGVLTVMNDTVLDGSDVTKNTTDTVATFSSVYG 199
QY 188 PLGMYVEGSKYWFRLPAKHTVNSEPDIKQISLPQVDIAVSYGNTDTYKALQNGAK 247
DB 200 PLGYTHNGKIDYQRTPAKHTSDPFPVSKINELPKVGI VVNYNAASDLPAKALVDAGVD 259
QY 248 ALIHTAGTNGSVSSRVVPAQLQELRNQVQIIRSSRQGGFVLRNAEQPDDKNDVVAHDL 307
DB 260 GIVSAGVNGNLYKSVFPTLTAAKNGTAVVRSRVPFGATTQDAKVDKYGFIASGTL 319
QY 308 NPQKRIILAMVAMTKTQDSKELQRIFWEX 336
DB 320 NPQKRIILQALATVTDPOQIQOIFNOY 348

RESULT 4
A58108
periplasmic L-asparaginase II [imported] - Escherichia coli (strain O157:H7, substrain R)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A58108
R:Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A59629; MUID:21156231; PMID:11258756
A:Accession: A58108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <HAY>
A:Cross-references: UNIPROT:O8XC2; GB:BA000007; PIDN:BA037256.1; PID:G13363305; GSPDB:G
A:Experimental source: strain O157:H7, substrain RMD 0509952
A:Gene: EC03833
C:Superfamily: asparaginase

Query Match 46.8%; Score 786; DB 2; Length 348;
Best Local Similarity 48.3%; Pred. No. 3.2e-46;
Matches 159; Conservative 59; Mismatches 107; Indels 4; Gaps 3;

QY 9 LANVILATGGTIGAGASANSATYQAKYGVDTLIGVPELADLANVRSQVMOQIASB 68
DB 23 LPNITILATGGTIGAGGSATRS-NYTAGKGVENLVNAVQQLDIANVKGQVNNISQ 81
QY 69 SITNDLILKLASSVAELADSDVDGIVTHTGDTLLEAFYPLNVEKTDKPIVVGSRP 128
DB 82 DMNDVWVTLTKKIN--TDCCKTQGFVTHGDTMEERAFPLDVLVCKDKPVMWGANRP 139
QY 129 GTAMSADGMLNLVNAVAVASNKDSRGKGVLTVMDEIOSGRDVSINIKTEAFKSA-WG 187
DB 140 STMSADGPFNLVNAVAVTAAKASANRGVLTVMNDTVLDGSDVTKNTTDTVATFSSVYG 199
QY 188 PLGMYVEGSKYWFRLPAKHTVNSEPDIKQISLPQVDIAVSYGNTDTYKALQNGAK 247
DB 200 PLGYTHNGKIDYQRTPAKHTSDPFPVSKINELPKVGI VVNYNAASDLPAKALVDAGVD 259
QY 248 ALIHTAGTNGSVSSRVVPAQLQELRNQVQIIRSSRQGGFVLRNAEQPDDKNDVVAHDL 307
DB 260 GIVSAGVNGNLYKSVFPTLTAAKNGTAVVRSRVPFGATTQDAKVDKYGFIASGTL 319
QY 308 NPQKRIILAMVAMTKTQDSKELQRIFWEX 336
DB 320 NPQKRIILQALATVTDPOQIQOIFNOY 348

RESULT 5

NCBI
asparaginase (EC 3.5.1.1) II precursor [validated] - Escherichia coli (strain K-12)

C/Species: Escherichia coli
C/Date: 24-Apr-1984 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004

C/Accession: A35132; J03030; A01000; D65081

R/Jennings, M.P.; Beacham, I.R.

J. Bacteriol. 172, 1491-1498, 1990

A/Title: Analysis of the Escherichia coli gene encoding L-asparaginase II, anB, and its

A/Accession: A35132

A/Reference number: A35132; MUID:90170867; PMID:2407723

A/Molecule type: DNA

A/Residues: 1-348 <JEN>

A/Cross-references: UNIPROT:P00805; EMBL:X52540

R/Bonthon, D.T.

Gene 91, 101-105, 1990

A/Title: L-asparaginase II of Escherichia coli K-12: cloning, mapping and sequencing of

A/Accession: J03030

A/Reference number: J03030; MUID:90382683; PMID:2144836

A/Molecule type: DNA

A/Residues: 1-348 <BON>

A/Cross-references: GB:M34234; NID:G145276; PIDN:AA23445.1; PID:G145277

A/Experimental source: strain K12 JM108

R/Malta, T.; Macneil, G.

Hoppe-Seyler's Z. Physiol. Chem. 361, 105-117, 1980

A/Title: The primary structure of L-asparaginase from Escherichia coli.

A/Accession: A01000

A/Reference number: A01000; MUID:80135739; PMID:6766894

A/Molecule type: protein

A/Residues: 23-48 'A', 50-85 'D', 87-131, 133-155, 157-170, 172-205, 'D', 207-267, 'D', 269-273, 'R. Peterson, R.G.; Richards, P.F.; Handeschmader, R.E.

J. Biol. Chem. 252, 2072-2076, 1977

A/Title: Structure of peptide from active site region of Escherichia coli L-asparaginase

A/Reference number: A3655; MUID:77140944; PMID:321449

A/Contents: annotation; active site

R/Greenquist, A.C.; Wriston Jr., J.C.

Arch. Biochem. Biophys. 152, 280-286, 1972

A/Title: Chemical evidence for identical subunits in L-asparaginase from Escherichia coli

A/Reference number: A37451; MUID:73007901; PMID:4561256

A/Contents: annotation

A/Note: the cysteine residues were quantitated and shown to form intrachain bonds

R. Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A., Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: D65081

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-348 <BLAT>

A/Cross-references: GB:AE000378; GB:U00096; NID:G1789319; PIDN:AACT5994.1; PID:G1789327;

A/Experimental source: strain K-12, substrain MGL655

C/Genetics:

A/Genes: anB

A/Map position: 64 min

C/Complex: homotetramer

C/Function: A/Description: EC 3.5.1.1 [validated, MUID:90170867]; catalyzes the hydrolysis of aspara

A/Note: has a higher affinity for asparagine than asparaginase I (PIR:XDC1)

A/Note: positively regulated by CAMP receptor protein (CRP) (PIR:Q8EC) and by PNR prote

C/Superfamily: asparaginase

C/Keywords: extracellular protein, homotetramer, hydrolase

P.1-22/Domains: signal sequence #status predicted <Sig>

P.23-48/Product: asparaginase #status experimental <Mat>

P.99-127/Diulfide bonds: #status experimental

P.142/Active site: Ser #status experimental

Query Match 46.0%, Score 772, DB 1, Length 348,

Best Local Similarity 47.7%, Pred. No. 2, 9e-45,

Matches 157, Conservative 59, Mismatches 109, Indels 4, Gaps 3;

QY 9 LANVILATGTTAGAGASAAATYQAKVGVKLIAGVPELIADLANVGRQWQIASSEIT 68

DB 23 LPNITILATGTTAGGGSATKS -HTYGVKGVENLVNVAPOKLOIANVKGQVNIISGQ 81

QY 69 STTNDLLKLASSVAELADNDVDGIVTTHGDTLEETAYFLNLYEKTDPYVVGSGMRP 128

DB 82 DNDVNDVWLAKKIN -TDCDCTKIDGFTVTHGDTMEETAYFLDLTVKCKPVMVGMAMP 139

QY 129 GTMSADGMLNLYNVAVANSNDRSKGVLYMNDIEISGRVSSINIKTEAFPSA -WG 187

DB 140 STSMADGDFNLNVAVNTADASANRGLVNMNDIVLDGRVTTKNTTVDATFSSVNTG 199

QY 188 PLGMVVEGKSYWFRLLPAKHVTNSERFDIKQISLPOVDIAYSQVNTDTAYALQNGAK 247

DB 200 PLGYIHNGKIDYQKTPARKHSDTTPDYSKLNELPKVGLVYNNANSDLPARALVDAGYD 259

QY 248 ALIHAGTNGSVSRVPALELRKNGVOIIRSSQGGFVLNABQDPDKMDVVAHDL 307

DB 260 GIVSAGVNGNLYKSVFDTLAAKGTAVVSSRVPTGATYQDAEVDAAKGFVASGTL 319

QY 308 NPQKARILLAMVMTKQDSKEIORTFWEX 336

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

QY 320 NPQKARILLALTYKQDQIQQIFNOY 348

DB 320 NPQKARILLALTYKQDQIQQIFNOY 348

Db 165 TTYGKVEYFQSVRPHLASEPDISKIEBPRVDILVAHPDDTDLVNAALQAGKII 244
 Qy 251 HAGTNGSVSRVPLQELARKNGVOIIRSSROQGFVLRNAEQPPDKNDVVAADLNPQ 310
 Db 245 HAGKNGNFPRLQALREKAAKSGVAVSRVSGSTTQBAFVDDKLGAFATSIANQ 304
 Qy 311 KARIILAMVMTKTQDSKEKQRIFFWEX 336
 Db 305 KARVILMLALTFTKSDREAIQKIFSTY 330

RESULT 7

Asparaginase (EC 3.5.1.1) - *Salmonella enterica* subsp. *enterica* serovar Typh1 (strain CT A80879)
 CSpecies: *Salmonella enterica* subsp. *enterica* serovar Typh1
 A>Note: this species has also been called *Salmonella typhi*
 CDate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 CAccession: AB0879
 RParthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, R.; Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AB0879
 A:Status: preliminary
 A:Statues: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <PAR>
 A:Cross-references: GB:AL513382; PIRN:CAD02930.1; PID:g16504183; GSPDB:GN00176 C:Gene: STY3259
 C:Superfamily: asparaginase
 C:Keywords: hydrolase

Query Match 45.3%; Score 761; DB 2; Length 348;
 Best Local Similarity 47.1%; Pred. No. 1.6e-44;
 Matches 155; Conservative 60; Mismatches 110; Indels 4; Gaps 3;

Qy 9 LANVVIATGTTIAGAGSANSATYQAKVGVKLIAGVPELADLANVGRBQWQIASE 68
 Db 23 LPNITITLATTGTTIAGGDSATKS-NTYACKVGVENLVADVPOKDIAYVKGQVANNISQ 81
 Qy 69 SITNDLLKLASSVABLADSDVDGIVITHGTDTLEETAYFLNVEKTDKPIVVGSMRP 128
 Db 82 DNMDEWVLTIAKKINTBCDS--TDGFVITHGTDTMEETAYFLDLTVCKNKPVLVGAARP 139
 Qy 129 GRMADNGLNLYNVAVASNDKSRGKGLVYTMNDEIQSGRVSKSINIKTAFAKSA-WG 187
 Db 140 STSMGADGPFNLYNVAADQASARGLVYVMDGVITKMTTDTVAIFFAVWYG 199
 Qy 168 PLGVVVGKSYFRLPAKHHTVNSEFDIQISLPOVDIAYSGVNTDTAYKALQNGAK 247
 Db 200 PLGVTHNGKIDYQRTPERKHTTSTPDDSKTALRPFVGIYVYANASDLPALQVADAGTD 259
 Qy 248 ALIHAGTNGSVSRVPLQELARKNGVOIIRSSROQGFVLRNAEQPPDKNDVVAADL 307
 Db 260 GIVSAGVNGNLYKTVPTDLTAHNGTVAVSRVPTGATTTQDAEVDPAKGVFASGTL 319
 Qy 308 NPQKARILAMVMTKTQDSKEKQRIFFWEX 336
 Db 320 NPQKARVILQALTLQTKOPKQIQTFWNOY 348

RESULT 8

Asparaginase (EC 3.5.1.1) II precursor - *Haemophilus influenzae* (strain Rd KW20)
 CSpecies: *Haemophilus influenzae*
 CDate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 CAccession: A64090
 R.Pletschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervlaage, J.; Goeyens, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritschman, J.L.; Fuhrman, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: A64090
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-349 <TIGR>
 A:Cross-references: UNIPROT:P43843; GB:U32758; GB:L42023; NID:g1573747; PIRN:AAC22403.1; C:Superfamily: asparaginase
 C:Keywords: extracellular protein; hydrolase
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-349/Product: asparaginase #status predicted <MAT>
 F:100-128/Distulfide bonds: #status predicted

Query Match 45.1%; Score 758; DB 2; Length 349;
 Best Local Similarity 45.1%; Pred. No. 2.6e-44;
 Matches 151; Conservative 74; Mismatches 106; Indels 4; Gaps 3;

Qy 3 VENQOKLANVVIATGTTIAGAGSANSATYQAKVGVKLIAGVPELADLANVGRBQV 62
 Db 18 IANAADLPNITITLATTGTTIAGGDSATKS-YKAGQLSIDTLIAVPEKNTIANIKGBQI 76
 Qy 63 MOIASESITNDLLKLASSVABLADSDVDGIVITHGTDTLEETAYFLNVEKTDKPIYV 122
 Db 77 VKIGSQDNDEWVLTIAKAIN--AQCKSTDGIVITHGTDTMEETAYFLDLTVCKEKPVL 134
 Qy 123 VGSNRPGTAMSDGLNLYNVAVASNDKSRGKGLVYTMNDEIQSGRVSKSINIKTAFA 182
 Db 135 VGANRPATEKSDGFLNLYNVAADKSSRGVLYVMDGVITKMTTDTVAIFFAVWYCF 194
 Qy 163 KSA-WGPLVVGKSYFRLPAKHHTVNSEFDIQISLPOVDIAYSGVNTDTAYKAL 241
 Db 195 HSPNYGSLGYIHSKVDYERSPEKHTINTPENVKLDLPVGIYVSNAPVPELNL 254
 Qy 242 AONGKALIHAGTNGSVSRVPLQELARKNGVOIIRSSROQGFVLRNAEQPPDKNDW 301
 Db 255 IMAVGQIVSAGVNGNVAHDLERKADSDVAVSRVPTGYTTRDAEVDSDSKYGF 314
 Qy 302 VVAHDLPQKARILAMVMTKTQDSKEKQRIFFWEX 336
 Db 315 VASGTLNPQKARVILQALTLQTKOPKQIQTFEDP 349

RESULT 9

Asparaginase (EC 3.5.1.1) yccC [similarity] - *Bacillus subtilis*
 CSpecies: *Bacillus subtilis*
 CDate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 CAccession: F69754
 R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertore C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erttington, J.; Fabret, C.; Ferrari, B. Nature 350, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Gallert A.; Iach, J.; Harwood, C.R.; Henuat, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogilawa, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, A.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumeitein, B.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:96044033; PMID:9383377

A:Accession: F69754
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-375 <KUN>
 A:Cross-references: UNIPROT:O34482; GB:Z99105; GB:AL009126; NID:g2632457; PIRN:CAB12063.1 A:Experimental source: strain 168
 C:Genetics:

A:Gene: yccc
C:Superfamily: asparaginase
C:Keywords: hydrolase

Query Match 45.1%; Score 758; DB 2; Length 375;
Best Local Similarity 47.6%; Pred. No. 2.9e-44;
Matches 158; Conservative 58; Mismatches 112; Indels 4; Gaps 3;

QY 6 OOKANVILATGTTAGAGAAANSATYQAAKVGDKLIAGPELADIANRGQVMQI 65
DB 47 KOLPVRILATGTTAGAGDQSTKTKAGVGVESILEAVPEKDIANVSGEQIVAV 106
QY 66 ASESTINDDLKLASSVAELADSNVDGIVTHGDTLEETAYFLNLVEKTKPIYVVS 125
DB 107 GSTINDKLLKLAKRINLILASDDVDGIVTHGDTLEETAYFLNLVYSKDEPIYVS 166
QY 126 MRPGTMSADGMLNLYNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFKS- 184
DB 167 MRPSTALISADGPNLNYNAVAVAGAPAKGKGLVVLNDIASRKYVTKTNTTTTDTFKSE 226
QY 165 AMGPIMGVVGKSYMPRLPAKHVTNVEPDIKQISLPQVDIAYSXGNTDTAYKALAGN 244
DB 227 EMGPFVGTAD-DIYFNNEITRRKTKDTDFSVSNLDELPOVDIIYQNDGSYLPDAVAV 285
QY 245 GAKALIHAGTNGSVSSRVVPALQELRKNGVOITRSSRQGGFVLNNAEQPDDKNDWVVA 304
DB 266 GAKGIVFAGSGNGSLSDAAEKADSAVKGIVYVRSRTGNGVVTNODYAR--KDLIAS 343
QY 305 HDLNPQAKRILAMVAMTKTQDSKEIQRIFWEX 336
DB 344 NSLNPQAKRILMLALTKTNDPOKIQAYFNEX 375

RESULT 10

AD0169
asparaginase (EC 3.5.1.1) precursor [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #ext_change 09-Jul-2004
C:Accession: AD0169
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Croxall, A.; Davies, R.M.; Dougan, G.;
11, M.; Rutherford, K.; Simmons, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <KUR->
A:Cross-references: UNIPROT:Q8ZGB7; GB:AL550842; PDB:CA090215.1; PDB:G15979435; GSPDB:C
A:Gene: ansp
C:Superfamily: asparaginase
C:Keywords: hydrolase

Query Match 44.6%; Score 749.5; DB 2; Length 345;
Best Local Similarity 47.7%; Pred. No. 9.8e-44;
Matches 157; Conservative 54; Mismatches 111; Indels 7; Gaps 4;

QY 9 LANVILATGTTAGAGAAANSATYQAAKVGDKLIAGPELADIANRGQVMQIASE 68
DB 23 LNTITLANTGTTAGGDSATKS-NTTAKGLGVDLVAENVPALIKDIANIGSGVNIISGQ 81
QY 69 SITNDLKLASSVAELADSNVDGIVTHGDTLEETAYFLNLVEKTKPIYVVSMP 128
DB 82 DNNDVWMLTAKKINK--DCTKTDFVITHGDTLEETAYFLNLVYCNCKPVIYGANMP 139
QY 129 GTMSADGMLNLYNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFKS-AW 187
DB 140 ATALGADGPLANTYNAVAASDADSAKRGVAVANDVTFGRDVKNTTTSVQTPQSPNTG 199
QY 188 PLGMVVGKSYMPRLPAKHVTNVEPDIKQISLPQVDIAYSXGNTDTAYKALAGNGAK 247

DB 200 PLGIYIDGKNTYIHPAARQLA---FDISKLNTLPRVGIINYVANAASDIPAKALADGYQ 256
QY 246 ALIHAGTNGSVSSRVVPALQELRKNGVOITRSSRQGGFVLNNAEQPDDKNDWVVAHD 307
DB 257 GIVSAGVGNLHYTFVDTLATPAASHGAVAVSSRSPSTTEGALIDDAKTGFVAAGAL 316
QY 308 NPOKARILAMVAMTKTQDSKEIQRIFWEX 336
DB 317 NPOKARILMLALTQTQKQEIQKLFHTY 345

RESULT 11

AZ6054
asparaginase (EC 3.5.1.1) precursor - Brwnia chrysanthemi
C:Species: Brwnia chrysanthemi
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
C:Accession: AZ6054; S03681
R:Minon, N.P.; Bullman, H.M.S.; Scawen, M.D.; Atkinson, T.; Gilbert, H.J.
Gene 46, 25-35, 1986
A:Title: Nucleotide sequence of the Brwnia chrysanthemi NCPB 1066 L-asparaginase gene.
A:Reference number: AZ6054; MUID:87106840; PMID:3026924
A:Accession: AZ6054
A:Molecule type: DNA
A:Residues: 1-348 <MIN->
A:Cross-references: UNIPROT:P06608; GB:M14741; GB:X14777; NID:942965; PDB:CAA32884.1; P
A:Note: the authors translated the codon AAG for residue 266 as Leu
R:Filipula, D.; Nagle, J.W.; Pulford, S.; Anderson, D.M.
Nucleic Acids Res. 16, 10385, 1988
A:Title: Sequence of L-asparaginase gene from Brwnia chrysanthemi NCPB 1125.
A:Reference number: S03681; MUID:89057497; PMID:3194219
A:Accession: S03681
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-176, 'I', 178-198, 'R', 200-287, 'U', 289-294, 'W', 296-348 <FIL->
A:Cross-references: GB:X12746; NID:940993; PDB:CAA31239.1; PDB:940994
C:Superfamily: asparaginase
C:Keywords: hydrolase
P:1-21/Domain: signal sequence #status predicted <SIG>
P:22-348/Product: asparaginase #status predicted <MAT>

Query Match 44.6%; Score 749; DB 1; Length 348;
Best Local Similarity 47.3%; Pred. No. 1.1e-43;
Matches 156; Conservative 63; Mismatches 105; Indels 6; Gaps 2;

QY 8 KLANVILATGTTAGAGAAANSATYQAAKVGDKLIAGPELADIANRGQVMQIIS 67
DB 24 LNPVILATGTTAGTISATYQTTGYKAGLGVTLINAVEPVKLANVKGQPSNMAS 83
QY 66 SITNDLKLASSVAELADSNVDGIVTHGDTLEETAYFLNLVEKTKPIYVVSMP 127
DB 84 ENMTGVDVILKSORVNELARDVDGIVTHGDTLEETAYFLNLVYSKDEPIYVVAAR 143
QY 128 PGTMSADGMLNLYNAVAASNKDSRGKGLVTMDEIQSGRDVSKSINIKTEAFK-SAW 186
DB 144 PATALISADGPMILLEAVRVAAGDKSRGCMVVLNDRIGASAYITKTNASTLDTFRANEE 203
QY 187 GELGVNVGKSYMPRLPAKHVTNVEPDIKQISLPQVDIAYSXGNTDTAYKALAGNA 246
DB 204 GYLGVIIGNRIYQURIDLHTTRSVFVGRGTSIPKVDILGYDDPEYILDALIQGV 263
QY 247 KALIHAGTNGSVSSRVVPALQELRKNGVOITRSSRQGGFVLNNAEQPDDKNDWVVAHD 306
DB 264 KGIIVAGMGASVSARGIAGMKAMEKGVVIRSTRINGIV-----PDDELPLGLVSDS 318
QY 307 INPQARILAMVAMTKTQDSKEIQRIFWEX 336
DB 319 INPQARILMLALTRTSDPKVIQEVFHTY 348

RESULT 12

H81418
asparaginase (EC 3.5.1.1) cytoplasmic Cj0029 [imported] - Campylobacter jejuni (strain NC
C:Species: Campylobacter jejuni

[illegible][illegible]

Db 301 DNINPQKARVLQLALTKTNDKAKIOEMFEEX 332

RESULT 15

T50284

asparaginase (EC 3.5.1.1) precursor [similarity] - fission yeast (Schizosaccharomyces po

C/Species: Schizosaccharomyces pombe

C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C/Accession: T50284

R/Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 2000

A/Reference number: Z25053

A/Accession: T50284

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-356 <ZIM>

A/Cross-references: UNIPROT:Q9UTS7, EMBL:AL137130, PTDN:CAB69634.1; GSPDB:GNO0066; SPDB:

A/Experimental source: strain 97ah(-); cosmid c977

C/Genetics:

A/Map position: 1

C/Superfamily: asparaginase

C/Keywords: hydrolase

Query Match 32.7%; Score 550; DB 2; Length 356;

Best Local Similarity 41.0%; Pred. No. 4e-30;

Matches 136; Conservative 56; Mismatches 120; Indels 20; Gaps 8;

QY 9 LANVILATGTTAGAGASANSATYQAAKGVGDKLIAGVPLADLANVRGEQVMQIASE 68

Db 35 LBNVTVFAMGTTIAGCANSLSLEIVNYIPGSVGIEKLIBAVPAIKAIANINGVQVTWNGSE 94

QY 69 SITNDLLGLASSV-AELDSNDVDGIVITHTGDTLEETAYPLANTVEKTDKPIVVGSKR 127

Db 95 NLTPLADVLLAKLIILAEVAKPN-VHGIIVTHGTDSLSEETAMFLDLTISTAKPIVVGAMR 153

QY 128 PGTASADGMLNLYNVAASNDKSRGKGLVTMNDIIOGRDVSISINIKTEAFKS-AW 186

Db 154 PSTAIGADGPMILNVAASNSQSGRGTLVILNDRIGSAFTTITKINGNTLDTFKSYEA 213

QY 187 GPLGNVVEGSKSYWFLPAKRHTVNSBFDIKQISLPQVDIAYSYGNVTDPTAYKALAONGA 246

Db 214 GSLGIVLQKPFYFSPAV-PTGKVFPFDIYNIKQLPRVDILVGYQGLNPKLASAVHLGA 272

QY 247 KALIHAGTNGSVS--SRVVPALQELRKGVOITRSSRQGGFVLNABQPDKND--W 301

Db 273 KGLVLAAMGATSWTDGNEVISL--IRRHNIPEVVSHTABGY-----SSNSCLG 321

QY 302 VVAHDLNPOKARILANVAMTKTQDSKELQRI 333

Db 322 IPSYPLNPOKARYMLMLAISGSYIRDIIDL 353

Search completed: March 18, 2005, 21:33:21

Job time : 43 secs

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